

*Supplementary Material*

# Genome-Wide Identification Analysis of the R2R3-MYB Transcription Factor Family in *Cymbidium sinense* for Insights into Drought Stress Responses

Mengjia Zhu<sup>1,2</sup>, Qianqian Wang<sup>2</sup>, Song Tu<sup>2</sup>, Shijie Ke<sup>1,2</sup>, Yuanyang Bi<sup>2</sup>, Sagheer Ahmad<sup>2</sup>, Diyang Zhang<sup>2</sup>, Dingkun Liu<sup>1,2</sup> and Siren Lan<sup>1,2,\*</sup>

<sup>1</sup> College of Forestry, Fujian Agriculture and Forestry University, Fuzhou 350002, China

<sup>2</sup> Key Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization, College of Landscape Architecture and Art, Fujian Agriculture and Forestry University, Fuzhou 350002, China

\* Correspondence: lkzx@fafu.edu.cn; Tel.: +86-139-0690-0395

## SUPPLEMENTARY TABLE LEGENDS

**TABLE S1|** *CsMYBs* protein sequences used in the phylogenetic tree;

**TABLE S2|** Ka/Ks analysis of *CsMYB* genes;

**TABLE S3|** Protein secondary structure prediction of *DrMYBs* and *CsMYBs*;

**TABLE S4a|** Putative *cis*-acting elements identified in the promoter regions of *CsMYB* genes;

**TABLE S4b|** The number of MBS elements in *CsMYBs* and 11 *DrMYBs*;

**TABLE S5a|** Expression profiles of *CsMYB* genes in leaves;

**TABLE S5b|** Expression profiles of *CsMYB* genes in roots;

**TABLE S6a|** The fold-changes of *CsMYB* genes in leaves of *C. sinense* under drought stress treatment;

**TABLE S6b|** The fold-changes of *CsMYB* genes in roots of *C. sinense* under drought stress treatment;

**TABLE S7|** The primers of *CsMYB* genes;

**FIGURE S1|** The 15 motifs of *CsMYBs* and *DrMYBs*;

**FIGURE S2|** The collinearity of *CsMYB* genes in *C. sinensis*;

**FIGURE S3|** RT-qPCR validation of transcriptomic data of nine *CsMYB* genes under drought stress;

**FIGURE S4|** The plant of *C. sinense* under three treatments.

**TABLE S1.** *CsMYBs* protein sequences used in the phylogenetic tree

Gene ID	Sequence
Mol004798	MGRAPCCDKANVKKGPWSAEDSKLKEFIEKLRWLNYLRPNIKHGEFSDAEDRTICTLFA SIGSRWSIIASQLPGRTDNDIKNHWNTKLKK KLLGISSSEKKNSLHHQQQSQHLLFSSPTPSLFSNPYININATSAPIQIPFLSGFSHQANLVPIPEGFSASSTSSSSCLFQSSQYQVKERGST VLAFFGESSDQGSCTQIRENMSLNNFLVYGTNTGFQDFCGLQSSAPLEECLSYGFDEIKQLLMNSNNGIFLEDQTVEGCNSQWKSMSTS* MSREINEGNRIEAPKDQFESSQNDESSCSRSSLAGGTVLKKGHWSPSEDAILVDYVKKHGEGNWNAIEKRTELRRCGKSCRLRWANHLKP GLKKGALTREEVEKIDQLHCKLGSKWAKIAAMFCAWLILLEILTASSSGIDSPKFMDALTYKPSHASDTSHFTVPNSILLPFDSLHLLSEN DSKGHSQAAA VRKQVTRESLARSHAVSNGLLPGRTDNEIKNYWHTRAKRYQRTCLPHYPQHVRQALDENQQLTNYSMSNREDKGLGI VLQSAMHDSAKFFKANPGPQAYSLPFDISFTGLQSQDLVSHTYSFNPGVNHAIQLRETESYFPGNHGSMASGHAMFEQLPHGPNPVNKN VPSFGYSEPGSLIQPNVNFS TSSPPTGTMKLEPLSLQYPETDCYSRLAYPPPLPYEAIHTDIQSLPMVVSTQPGYTSQSSGLSETLVQVSHAIST VGKQSSSEKSSNYS AISPIDILENSSPNMCSADWKSGDPNSPFLPEVSPFSECLPIDDISFDDFVDSEATLGHDLCLK* MLPSIINQPRSMFMDN ASIAATSFISIFIVGFAAAGQHGWT FEDGWRKGPWTPQEDKLLTEHVKLHGEGRWNCVSRLTGLRSGKSCRL RWVN YLRPDLKRGKITPHEETIILELHAKWGNR* MFILRQVDGV DLLIESIPHANPFRCRMRLRTCEQKVSVRKG LWSPEEDQKLKNYTAWPWMLELHSLS CRLRWINYLRPGLKRGIFTSEED
Mol028264	IIMSLHAKLGNKWSRIA AHLPGRTDNEIKNYWNSY LKKLMQQNHQPMISSNELNESIQ QTSKSENFQLESINQSATSSCSIDNGSFKSSFP RVLFEWLSPQDMGRDEF DENG LLEEMQSLDMFGEMIGDIDMNYDFIH* MGRSPCCDEN GLKKGPWTPEEDQILVLYI QKHGHGSWR ALPKLAGLNRCGKSCRLW TNYL RPDIKRGKFSPEEEQSILHLHSILGNKWS AIATHLPGR TDNEIKNFWNTHLKKLIQM GFDPMTHR PRTDFFAALPHLLALANLVDHRPSTWLADGLSAEASKLQCLQYILNAATPTSA DNSMNNLLNSTDQSFSSLD MNSNQPLFNT HNT EIDVPLSYDQPLMSNENSGFSLFRHGEISTPV SALPPLTDLSNPGDAC STSSCGGSAAA SFWPDLLLDDPFMAEFA*
Mol003923	MGRVPCCDKDGLKKGPWTPEEDQKLIDYI QKHGHGTWRTL PKNAGLARCGKSCRLW ANYLRPDIKRG RFSFEEETIIQLHNILGNKWS AIAARLPGR TDNEIKNYWNTHIRKRLRNPGDTPAPARSP* MCSRGHWRPAEDEKLKDLVT KYGPHNWN AIAEKLPGRSGKSCRLWF NQLDPRINRSPFTEEEERLLTSHRIHGNRWSVIARLFPGRTD
Mol013646	NAVKNHWHVIMARKVRERSRFH GKRPCFSSSLIMGDSSSNAQGKQ GSLQEPQGFFSLVGNCYKKQQNCFLGDFRSNSDEFQSWIHGFS GDFSLVGKKNPIFYDFLQVNSDSNGTKCSSVEDEKDEADQQEQSKARPFFDLPVNGSI*
Mol018713	

Mol017692 MGRPPCCDKVGVKKGWPWTPEEDINLVSYIQEHGPGNWKAIPNTNSGLSRCSCRLRWTNYLRPGIKRGSFTEQEENLIIHLQALLGNRWAAIASYLPERTDNDIKNHWNTMHMKKLRMENEKKLGGMIAGSGFSKNQSIAKGQWEKRLQTDINMAKQALQEALSMEKPSFLYESKPSSSHSSSTPPSSTTYASSTENISRLLENWMRKAPKNSDKSTQHSVKNFVNIGADSTSSDGTITSVANNHIVSPEISQFQVDSKPCCLDERFPLSLIETWLFDENYWGGNGSNNVLDFSFDDASHELF\*

Mol011788 MCTRGHWRPEEDEKLKELVARLGPHNWNTIAEMLHGRSGKSCRLRWYNQLDPRINRCPTEEEEERLLASHRIHGNGRWSIIARLFPGRTDNAVKNHWHVIMARRSRERSKLQTKQSSLLESHLVRKEKKEIMNFEFSKGFLFSSLIGEGRSRTLCAFKHPIQSQEVHSYSPNFHEAEGDTMESSIEFYDFLQVKSDSNETGECSRREDERDQNEKEQQCEAGVPFIDFLAVGS\*

MSSDADPMAVDETPPRPPPLENASSSSPSSPSSASIECAGPQAEGFGMKSGAASRDRVKGWPSSPEEDAILSRLVAKFGPRNWSLIARGVPGRSGKSCRLWCNQLDPQVKRKPFTEEDRIIIAHSLHGNKWAVIARLLEGRTDNAIKNHWNSTLRRKCIIESCKRAPCEGQEDISADILEKTKGSEETQSFGDVKPKFTGTEVRDISSRESLSHHSEDRVNTVGPEFKQPPTISRPVPRLSAFSPYNPGSHATSSLQSRSPLNAPHFRACLSGPGDYKLFENMLWEPQVPSRCGHGCCGTKTRDQNTSSSLGPEFVEFIEPPPILNREIASMAELSNIAWLKSQLQTGIYSSCQMNPPSSSCTASTC\*

Mol019840 MVVTREGIRKGPWTEQEDLQLVCFVSLFGERRWDFIAKVSGLNRTGKSCRLRWVNYLHPGLKRGRITPQEERLILDLHSQWGNGRWSRIARRLPGRTDNEVKNYWRTHMRKMAQESKRCPPRSSCSSESEQLEGDNGMEKNEQRSNMMPKNLEIKEEYEVKVYPMDQIWNDIAATLEPTTTSGLSFESYGHEAGNVSCVSAAMASPWWENCAESLWKMDDDELCVGIKS\*

MAFSSSAPQFSTVETQGRRNEAVLILEEQRVKRSSDFEGLSEKNGRIEDQEGIELESGHSKLCARGHWRPAEDAALKDLVAQYGPQNWLIAEKLEGRSGKSCRLWFNQLDPRINKKAFTEEEEERLLSAHRLYGNKWALISRLFPGRTDNAVKNHWHVIMARRQREQSNAYRRRKPC

Mol022732 TSSKIFHKRMEAKCSNNVCSAESTVSSNNHETLCINRSFPVHGFLTRYSPQQPQQFEYLFDTQGELVAGRSGCFERLFDSAIDMRQASPLIVVPGIHSGFSDNSEASASDSAINNAFISEEEAELESED\*

MVRVPCCDKDGLKKGPWTPEEDQKLIDYIYQKHGHTWRTLKPKNAGLARCGKSCRLRWANYLRPDIKRGGRFSFEEETIQLHNILGNKWSAIAARLPGRKDNEIKNYWNTHIRKRLLRSGIDPVTHQPRLDLLNLSSLLNTVLFNQSARLDASKLVDIKPHLNAKFRLRIA VSSLQSQYQKQNLLKHNLFQQSHPNCHQTITQPLPSSFLYNPVQFNAGQWQYNEESSCNLSNLNYENMAQSMTGLHGAFNAEIPSCQNLYSSLDSVLSTSVSSVTLNNSSIISNIEDEKIPTAATSLISRFLSC\*

Mol008801 MAANDVDRIGPWSPEEDEMLQILVEKHGPWNWSLISKSI PGRSGKSCRLWFNQLSPKVEHRPFTPDEDETIISAHRRFGNKWATIARLLSGRTDNAIKNHWNSTLERKEAAAAAAVAWTSEERMMGALEDCRPIKRSNGARLCFSPGSPSGCDDTGPTKRNYPQPSSLQVGKVIKADAP

Mol013522

DSTTGKWNPCDPFTFLTLSPGSSCGQNESSDNQKQTDPQLLEKKPPSVMASPFSLEFLEALQEIIHQEVKNYMSGLEHRGILPPPLPPEEDS  
KLNSVAKGIGISRIN\*

MVRSPSREERGLKKGPWTPEEDQKLIDYIQQKGSHGWRQLPRIAGLNRCGKSCRLRWTNYLRPDIKRGNFSEEEEKLIINLHSMLGNKWS  
LISTKLPGRTDNEIKNYWNTHLKKLLLGMIDPVTHRRTDLELFANFPKLLSSSTDSCSLINPLMENSLGLQADTVQLARIHLMQVLQVL

*Mol001350* LKAASFSSSSSNPNAYSNLVNNLMSSSLPPLETFSNNSSSSLPLETSAGFGEPSQTPTNYQDFNVQNSENISKQLLFHSNTNDLFASSENHS  
VDQKQDQIDLNETSAAKSVNTRYLDTLNLTDLDDTDLSWKDVLEPAETLHAKGSGSHCWLISPNTLSLLFCLVHSPCRSLLNRLLSGGVL  
T\*

MGRSPCCEKVGLKKGPWTPEEDQKLSSYIEEHGHGWRALPAKAGLQRCGKSCRLRWTNYLRPDIKRGKFMSMQEEQTIIQLHALLGNRW  
SAIATHLPKRTDNEIKNYWNTHLKKQLAKMGIDPVTHKPKSDALASADGHTRSTANLNHMAQWESARLEAEARLVRESKLRSSAPPSPFP

*Mol010990* PQYLPQPPPVSMPAAASPVDVLGAQGEWPKVVSQAGSHNIDLESPTSTLSFSENMLPSRIPGMGTANDSTNWKCLKPGFSLDTAE  
AFVNAEATSWLTGSCSGGFAAGFTGMLMGNTNKQNSTEGCDDSDIAGGSCVDVEEGEDEAEENKNYWNSIFNLVNSSSPNSPPAVF\*

MGRYPCCDEVGVVKKGWTPEEDQKLVEYIKENGHGWRHLPKSAGLNRCGKSCRLRWTNYLRPDIKRGKFSEEEERLIIHLHSVGNKW  
SSIATRLPGRTDNEIKNYWNTHLKKLLFMGIDPVTHRPITNIDLIANLPNLLSHTNLKNLAISCDQSLHQLHTDAAQFARIQIIQSLLHILSSP

*Mol001512* HPTYPADILLQLMNTKLEGSQLVAGQGLMPNNIEGLKQSSNGFDYQEIASKIMDDISKQGELFSSNTGGAAAANYSFPSLVSSSPENISV  
DQKQLEQIISNSSVAACSSSTPFDAWDGLHFSDQDAELGWKDILE\*

MGRSPCCEKAHTNKGAWTKEEDERLITYIKAHGEGCWRSLPKAAGLRCGKSCRLRWINYLRPDLKRGNFTVEEDELIKLHSLLGNKWS

*Mol008437* LIAGQLPGRTDNEIKNHWNTHIKRKLLNRGIDTQGTHPIAKAATAAPSKPTSMSAANTQQSMAEDEDAAHKNWQGLPDLNLELTISLPATS  
QMPVASRDNSTQSTCLCYSLGFPSISLACSCNMLQS\*

MLDDGRPSGVRIISDDGGDRRDAGYYGAAGKRRGVASKQPETPRPRQGRLQRWSAKDRDLAAWRDRHGYRRGCWVNQQQSRSLHPPPP

*Mol014848* LFPSERDGKTNETAFPLEQQQQPSLIGWGLEFGSGGSYGSEKNGQSEEHDGEHESGQSKLCARGHWRPAEADKLRELVAQYGPQNWN  
LIAENLEGRSGKSCRLWFNQLDPRINTKAFTEEEEERLLSAHRLYGNKWALIARFFGRTDNAVKNHWHVIIARKHRELSNSHRRRKASS  
SISSSAQAFDKNLQVNCYNNACIVESTISRNIDEFSTCTDLSLNSYAYRSFPGDGFFTRHIHEKQPQQFQYLTGSDEKAVTGRYGYSQRPFD  
SENDFRQVSPLVFVPGTYQSGYSDSNPEASATGSVVKGNAFIVEEGDNDREKISLPFIDFLGVRAT\*

*Mol018189* MGRPPCCDKIGVKKGPWTPEEDIILVSYIQEHGPGNWRSPVTNTGLSRC SKCRLRWTNYLRPGIKRGNFTDQEEKLIIHLQALLGNRWA  
ASYLPERTDNDIKNYWNTHLKKKLIRKLEIDVETEGESSLKRGASISNYQSVTKGQWERLQTDINMAKQALQEALSMEKPSFLYEIKPSCS

SHSSNNRSRSPSSTYASSTENISRLLQNWMRKPPNSSSSDRNSAESTQISVTANSSTVGKTVSGNDKRSSIVSPETCSLFQVESKPSLEPEL  
HFSQLETWLFDENYVGGTESSMNMLDLALDESELF\*

Mol010343 MGRSPCCDEVGVKKGPWTPEEDEKLVEHIKKHGHSWRHLPRNAGLNRCGKSCRLWNTYLRPDIKRGKFSEEEGLIILHSMGLGNKW  
SLISTKLPGRTDNEIKNHWNTHLKKLLIMGIDPVTHRRRADLEFLANLPNLSSNSCNRMTNSWGSALQLQAADAANLAQVQILQGLLQ  
VLIASSNSNSSNLSNMTNLLGSSLAPLRNIADILQVSQRQLEALQNGSFGLAHGSLPATTQMPNNYQTLPHQDDQPEVNGNENQNLLFHSNAP  
SLVSASPENTPSVSLKQEHIRSNEISAANSESSTPFDPWDALSLSDPNGADLGWKEILE\*

Mol001031 MSITPVEKFVMEKSERNPYAMKADTELRFYQRYYDDLISSGDTSFINTSEISSSTVEAKRGKSSSSSWAVSSVLTTSRTSVRGQWTAEEDNL  
LVKLVKEHGVRKWSQISKKLVGRIGKQCRERWLNLHRPGIKETWTEEEEISLIEHKELGNRWAEISKKIPGRSENSIKHNWNATKRLSSK  
RKGGIRKTSGKTSLLQEYIICKTELLNNSTSPKQQILPTTQTKVSDLNFLNCEHYFNGSIEDQIDFIDTSLPQFNELFEKEGNGSNGEFCSDV  
YLTHHMDEVPVVAPEFVNLLGENLKDFLGDDMDLECKKDMDLMEMILTCSSQEYPYNFGRSSSDSSLT\*

Mol012137 MTPSVELKEEPAVTPPETSAAVAGTAEASQLKKGPWTAAEDAILIEYVKKHGEGNWNAVQKNIGLQRCGKSCRLWANHLPNLKKGS  
FSPEEEALILQLHAQLGNKWARMAAHLPGRTDNEIKNYWNTRIKRRQRAGLPLYPPEIQYQLALMNQKQGNLMLHQNQIRPKNFMISHISP  
TTTTLFNHSGTSNNNTNYLLGNSNLNPPPHQLQSSTFSVKTELPSTQLFSCCAGDQKLLPPPVLТИEGNNVLFDDLYRESQGSGEFLNEG  
FFEPLSINCITTAESMPPQLPPPSNSKHSIIDPPYKLENSDITIGMQVMQPIETMVSQDVNCNPKMNMFTTMMPAEKLLSDWCELSPSAGV  
TEDDIRVEMQQLASTLSMNNDWNFELSSWQNMPDIR\*

Mol003893 MGRSPCCDKAHTNKGAWTKEEDQRLVSYIQAHGEGCWRSVPKAAGLLRCGKSCRLWINYLRPDLKRGNFTEEDELIKLHTFLGNKW  
SLIAGRPGRTDNEIKNYWNTHIKRKLRSRIDTQTHHPITATSAAFLSSPEIYSAVPESAVENTSDHKCHGSSSGGGSGNCADLNLELSISLPY  
YSSPQPSPYSDDASTAAAVRTPETCFCYRLGFRGGEACVCESLKEQVVSGLAMSD\*

Mol017415 MDGGGGGEEKIKGSWSPEEDALLMKLVERHGARNWTLISAGIQGRSGKSCRLWCNQLSPEVHHRPFTAEDAIIVAAHGKYGNKWATI  
ARLLPGRTDNAIKHNWNSTLRRRRRVEAATVSALSGPESESDSGGKRPCRRDDLILKVVEPMTPDAVDPATSLSLSPPGESSAAVAASAAT  
APDAGTGGGWKEKGWLGNACVMSVMRMIAEEVRRYMSGRLRDGGGFYSIVKAESASNGQD\*

Mol008800 MGRVPCCDKNGLKKGPWTPEEDQKLIDYIQKHGHTWRTLQPQAGLRCGKSCRLWANYLRPDIKRGFRSFEEEEAIQLHSILGNKWS  
AIAARLPGRTDNEIKNYWNTNIRKRLLRSGIDPVTHRPRLDLLNLSSLLSTVLFTQPSRLDALKLDDNKPQLNTEFLRIAANLLMSQCQHEN  
LFEHNQVQESQPTYHQTIQQQLSASLLYNPVEFSNTSQWQYNEASSCSLSDNLVTINNDLRYEASTVELPSDQNLYSQLDSVLSTPVSSMTM  
NDSSTAFNNSIEEKDSYHNDFFDFQISDMILDINEFI\*

Mol004182 MGHHS CCNQQKV KRG LWSPEEDEK LIKYV TTHGYGCWSEVPDKAGLQRCGKSCRLRWINYLRPDIRGRFSPEEKLIISLHAVVG NRWAHIA SHLP GRTDNEIKNYWN SWIKKKIRKPNTGTCSSSSPQCSVQILPTLIPGFNSLNQFEPLANQTLTNSKPNDNSNP IFPSSPIPLFMFDSEC  
GGTVAKEDHELLDVGNLNLVDWWTNDNQNDHQVLSPLSTFVDQNYLPP LVDSMVAMVPPP GCIGEECEASGSQECFEKNELSEWVEA  
QQYPGFFIWDQTVQGQLGGDELPVSTPP TSNTDASVDSFPSTL\*

Mol009531 MGRSPCCEKAHTNKGAWTKEEDERLVAYIKVHGEGCWRS LPKAAGL RCGKSCRLRWINYLRPDLKRGNFTEEDEL IIKLHSLLGNKWS  
SLIAGRLQGRTDNEIKNYWN THIRR KLLSRGIDPATHRPLQGP GDVS FVKADEKGASL IRKEDEQKSNNSSSSNSNSR SSSDEPKRWRC PDL  
NLELGISPPSHQEEDSEEDLMREELGLCFRNGLLEFR\*

MSSLQQRSEAPVLLSSLWPQASFLTASESPSEREVRSKESWSFNTSHDDLRLSDESMESRDLETQSKLCSR GHWRPTEDAKLKDLVAQ  
LGPQNWNLIAQNLKGRSGKSCRLW FNQLDPRINRKAFTSEEERLLSVHHHYGNKWSLIARFFPGRTDNAVKNHWHVIMARKQREHSIS  
YRRRLSSSTS FNPSPHLQTMEH NSSGESTITNTREEISSATTRTVHGLV LSPHQKKAINFIMGAKSIGDQITSSDSTS KASAREAVVFGSE  
LDRERINPPFFDFLG V GAA EKPL PVCVM PRERERES\*

Mol004081 MGRSPCCEKAHTNKGAWTKEEDERLTAHIKA HGEGCW RS LPKAAGL RCGKSCRLRWINYLRPDLKRGNFTEEDEL IIKLHSLLGNKWS  
LIAARLP GRTDNEIKNYWN THIRR KLMSSGIDPATHRPLNEQQEKTTISFIK GEEKVEEFEGREEGKSSNSSEEMS A WIRR PEEENKQW  
RCPDLNLELCMSPPSLKQQALCQEPVKSEELSFCNCRLGVNKSSDCKGSGFLGLRSGVLDYRRLETN\*

MGLKKGPWTPEEDRILVSYIQRYGHGNWRALPKQAGLSRCGKSCRLW TNYL RPDVKRGDFSKEEEETIYLHAMLGNRWSAIAAKLPG  
Mol013321 RTDNEIKNVW HTHLKKR LNPQAMKDSKRG NRNA MNKEMKKD MEDQVSPAC SRSEASSFVIATENCDVWWKEDSMDFL KELPE LD  
EILTS DAQSASQNNWAGEEEEE D STGKN YDRTRSSNEEDIRFWMNLLAEAGNLECFK\*

MGRSPCCEKAHTNKGAWTKEEDERLIAHIRAHGEGCW RS LPKAAGL RCGKSCRLRWINYLRPDLKRGNF TDDEDEL IIKLHSLLGNKWS  
LIAGRLPGRTDNEIKNYWN THIRR KLLNRGIDPATHR PISAAS TSNLSISFSSSSVT DKRNGV SRV SALLPRCPDLNLDLCISPPLEQLQQDL  
LEESNC GGEFLRGSSFL LDYRSLEM K\*

MGRPPCCEKEGVKKGPWTPEEDIILVSYIQEHGP GNWRAVPTNTGLMRC SKCRLW TNYL RPGIKRG NF TDQEEKLIHLQ ALLGNRWA  
AIASYLPERTDNDIKNYWN THLKKKLQLSGEDGGGRTVN PISNNHHQSFSKGQWERRLQTDI HMAKQALSEALSLDTMNL RSPSPS  
LGPANACTYASSTENISRLLENWMKSTPKRSRTSLGMSNV CSDSTMESTTPAGQIMTSSAVQLGFRPAKIEPNGVLKEESKE SVVA  
PPPLSF NIENWLFDL SVNGGDDHQDLV DPLPLSDA ESELF QD\*

Mol017976 MGHHC CSRQ KV KRG LWSPEEDEKL VRYITTHGHGCWSSVPKQAGLQRCGKSCRLRWINYLRPDLKRG SFTEQ EER VIIDVHR ILGNRWA  
QIAKHLPGRTDNEVKN FWNSCIKKLIAQGLDPKTHN LIPNTRPPYINSTS NIPHFPCQNTCIPFTI SSNIKETDS GRMMPL QTSS DALALHDSV

AISTFQYEDPDVMMSFKEHNSHEYNISASSSSLDHANILQISPNCDFMDDHCLWASSTPLEEAILADESKQNGERQQGEVQLGDKV  
DQFNEAMINGDASFDELMESELMPCGSVFCSDNSMEQLQWEC\*

Mol015419 METEKQNAIVEVDLRRGPWTVEEDLILTNYISKHGEGRWNTLAKCAGLKRTGKSCRLRWNLNYLRPDVRRGNITVEEQLLILELHSRWGNR  
WSKIAQHLPGRTDNEIKNFWRTRMQKHANQQCMPPLLERIRTVVDSSRAVMGVHTASASSGRNGFSSSATSNYDDHDLKDMASTLE  
EEGWPEFPAHGCEGSMMLGFWEFSAMGPNMYA\*

Mol026352 MAASEEMRKGPWTEQEDAQLVCYVHLFGERRWDIAKVSGWRCGGSRSLCFTGLNRTGKSCRLRWNLNYLHPGLKHGRMTPQEELIV  
ELHSRWGNRWSRIARRLPGRTDNEIKNYWRTHKRKAQERQSSLSPSSSSSSSSLNSIVMPDAKKA\*

MVRAPCCEKMGKKGPWTAEEDQILISIYIHNGHGNWRALPKLAGLLRCGKSCRLWTNYLRPDIKRGNFTREEEDIALLHQMLGNKW

Mol015023 SAIAAKLPGRTDNEIKNVWHHLKKRLKKTDTETTQEPKRKTQIESNEETTHSYSSIDVSCSGATESSTSSTVENSQNSMESLNHEFEEIDE  
SFWTEILQMESNGDYNDSIDSMATEEFSSDFMDETSLLSAGSRDEDDMNFWLRFVFLQAEELPEI\*  
MEIEVHGGATPHSEEEMELRRGPWTLEEDLVLMNYISSHGEGRWNSLARCAGLKRTGKSCRLRWNLNYLRPDVRRGNITPEEQLLILELHS  
RWGNRWSKIAQHLPGRTDNEIKNYWRTRVQKHAKHLQCDVDSKQFKDVMRYLWMPRLIERIRAASGNSAAQSVAGYGTLPGDDHTF  
GAATGWGGHGEIVKPRPESPATTVSSSGAGGYEVTEKPKDGEIQVNVPQHISGLWPEASLPTPGYAHQGIPELEQYWGLGDISDNLW  
SMDDIWYLQQ\*

Mol007990 MGRSPCCEKAHTNKGAWTKEEDERLIAYIRANGEWCWRSLPKAASLLRCGKSCRLWINYLRLPDLKRGNFTEEEDELIKLHSLLGNKWS  
LIAARLPGRTDNEIKNYWNTHIKRKLISRGTDATHRPLHEAQANNTISFFKGENKIVEVKREDERNKSSSSSSCCSSNSSEKLLIWRSEED  
DDEKMKWRCPDNLNELSISPPFEKKEDLCDYNVLNGEALIGLCFSCKLGVKNSSECKCGVFLGLSRGVLDYRSLETN\*

MGRGRAPCCQKVGLNKGWSWTVEEDQRЛИYINKNGHENWRALPKLAGLLRCGKSCRLWINYLRLPDIKRGNFTKEEEDIINLHELLGNK

Mol010269 WSKIAAHLPGRTDNEIKNVWNTHLKKRLNLKNFTPPSPTSMTKLHDDLSPTSSSTSISLSHETNSYSIDEETPFLDEIDNIIDPHLDMWDIF  
DDISISTSPPVMTITNDPNNTLDITMKECKQWLADLEEELGLYIDSVDDGDEIKGSEGEDLVRNYFHRGPSSPSSIRASRS\*

MGRGRAPCCEVGLNRGAWTPEEDMRLIAYIRKYGHGNWRALPKQAGLLRCGKSCRLWINYLRLPDIKRGNFSAEEEETIKLHGLLGNK

Mol010337 WSKIASSLPGRTDNEIKNVWNTHLKKRLKSNEQSSSSPTPIVSTTNPEDTQSSSSSSTSISIEHKCSHPCQDHSTDIPLLPNLDALDADLV  
DIEPKITDLADDLKDSIDEIIIGIDIEPEVWNDVVFTTEEACHEAEKRRWLAYLEEELGLFDDNVLASMMTRWWRWLWWVKGIP\*

MGGSDTNEVLEEDNNRADAEEENVNDCTGQSNLCVRGHWRPEEDCKLKLALVSIYGPQNWNLIAENLEGRSGKSCRLWFNQLDPTINRS

Mol028471 AFTEEEEEKLMAAHRLYGNKWAMIARLFPGRTDNAVKNHWHVIMARKYREQSTAYRRRKLNQAMDRRSEIIPNHPFSFSSSIADCSTYL  
HLLPNDGKNSSLHAGSYTREKLFDFLSGQNPSNGDKTKNFITRTWKKGKIIMKP\*

MRLRTCEEQKVSVRKGLWSPEEDQKLKNYMLQYGHGCWSSIPAQAGLQRNGKSCRLRWINYLPGKRGIFTSEEEEIMSLHAKLGNK  
*Mol011449* WSRIAALPGRTDNEIKNYWNSYLUKKLMQQNHQHPMISSNELNESIQQTSKSENFQLESINQSATSSCSIDNGSFPRVLFEELSPQ  
DMGRDEFDENLLEEMQSLDMFGEMIGDIDMNYDFIH\*  
MRRERACLPKEELRRGAWTEHEDKLLSDYITSHGLGRWRSLPEKAGLNRCGKSCRLRWINYLPGKRGNTDEEEELIIRLHKLVGNRWS  
*Mol012178* LIAGRIPGRTDNEIKNYWNSYIKKKVAMDVSSEHSYSKAATTAAAATTTASTTQLSFKSPCSEKANEASSVTSMVSKTYEAEDLNTNS  
AVLHEQHSSMKPEGHQVCLPPSASSDFDSGFESFGELSNSSVFSCYGRDAKSMACSSVIGEDCSSRRMEER\*  
MGHHSCCNQKVRRGLWSPEEDDKLIKYISTYGHGCWSSVPRRAGLQRCGKSCRLRWINYLPGKRGNTDEEEELIIRLHKLVGNRWAQ  
*Mol006542* IAKHTGRTDNEVKNFWNSTIKKKLISQAVEGLSIPNLSNQFPLHPQDLVPISSFQFHISHFQDQSQPYNFPNLAQMYPQTPQHNNMENPT  
VPHFLQLSSSYGPVWPFYQQEQQQPHQTYNHEPAMLFDENELQFFTGSLLDKKVEIAIDNQLVVTDLECFSSLSSMPYLESSHGYNGL  
MEYMHVLTGSDSLAEVTTEDHNSNDTFIQPYLLP\*  
MVLSRKKLKKKFRSLLAESVAADELKDSRKDALSAAEVNHELQIVRELLVSKSRRPKLLKRGNRGNKKPLDDSKNGDGSCARQGSVE  
NEGSIDLKDKGDKKRKRVEDGVLEEEGFKKEEQKLEKKKKDKQKKKKQREMKLKKKGKEEVEGKEETINVDEINMNGVSKIPEVVP  
VQVDESESKKVYVGPIPYYSSSEDIRSFFEDCGTVTEVDCMAFPETGKFRGIAILSFKKTQGKIPPLSISSSDPADPSIASQAVSDVRPASLL  
*Mol021224* QPLTRSSVGLPQDPFHHRCQFGLGSRLRTCPDPWTRAHHCFMPSDLRAVIHGISERLRTQDDLFRPEGAAKRALALDGSDMGGFFLKTQ  
PYKANRNQKSDFAPEIIDGYNRVYVGNLSWDISEDDLKQFFSDCKIASIRFGTDKETGDFKGYAHSKASSIVSSIHTKDKTRTLMVAMKEG  
TRKGWPTEQEDLQLVCCVSLFGDRRWDFIARISGLKRTGKSCRLRWNYLHPGLKQGRMTPEEEHLILELHSKWGNKWSQIAGKLPGR  
DNEIKNYWRTHMRKMAQEMKRNSQHSSSSSTSSSCLSLKTSTNGMENQQEVSFLLTMPEEKRR\*  
MGRSPCCEKAHTNKGAWTKEEDQRLIAYIGAYGEGSWRSLPTSAGLLRCGKSCRLRWINYLPGKRGNTFEEDELIKLHGLFGNKWS  
*Mol000543* LIASRLPGRTDNEIKNYWNTRIKRKLHDHGIDPQTHRPIASATRPPVLVNPADLFATTVITKLDERSHSEGSSASCTIDLNLDSIVSLPHSS  
VDDTPLTHSVTTSTMTTKMAATPAICLCYSLGFRGSEECGCQAVQEQQAVIRYCSSIEMLRNYFS\*  
MDLGSNLLILGESDLVFLVLGDLQGELDLEGIGGGGDSGVRERESLSIKILTLCFTWIEGKQERTQVMGRGRAPCCQKIGLHKGSWTPQE  
*Mol001517* DIRLISYIRKHGHGNWRALPKQAGLLRCGKSCRLRWINYLPGKRGNTFEEDELIKLHGLGNKWSKIASCLPGRTDNEIKNVWNTHLK  
KRLRHNNHPTQSPTNMAARPEVDAPSSSSGTAVTEGEELSFNKIEIPIEPQLDMWDILDSSLSPNLSPLPSPPPVEDDDILSDIPIDPDLWSDD  
TNIDSKTKEVDNSVGGKSADESKNWLAYLEEELGLFDEVETKETVELISMQVGEESMGSYFHKRPSSSSSTSLLTVDTVVHMSPWSN\*

MEGQYGWGTLEDGWWRKGPWTPQEDKLLTEHVKLHGEGRWNCVSRLTGLKRSRKSCRLRWVNLYRPDLKRGKITPHEETIILEHAKWG  
*Mol006174* NRWSTIARSLPGRTDNEIKNYWRTHFKKEKTMKNIERARANFLKQQQEQQHQQLQLEVPQFEEIAITQLMQEIAYMCNMPSVFQDE  
EFTSKSMVSSDDRLGDEAYYATSENWLNLDDLGLDMGDQALPFYY\*  
MVRAPCCERVGLNKQWTPQEDKILITYIQTYGHGNWRALPEKAGLRCGKSCRLRWNTYLNPGIKRGNFTKEEEDIINLQQILGNRWS  
*Mol020712* AIAAMLPGRTDNEIKNVWHHLKKRLNPQILQNSKRKIERRDRNSNSVIEFSSTSASESCSDFSSPTTESSNVSERDNSNSRNDSTCDNG  
VEEIEESFWTEILFVNGCDSPLMEVDSSKNEDLSFWLRIFMEAETLQGFPEI\*  
MDMRRGPWTMEEDLILMNYIAMHGEGRWNSLARCAGLKRTGKSCRLRWNLQYRDPDIRGNITPEEQFLILELQSRWGNRWSKIAQQLPG  
*Mol002558* RTDNEIKNYWRTRVQKHAKQLQCDVNSKQFQDVWRYIWMPRLMERISVASGELPAACMNLQTDTIGCKQCETGPEISGCTGSCSEST  
GSIGTTSTEGKPECDRSLGSSGTHNHDVCPWPEAAPQNPTGYAYEQELPELDQYWGGEEYENMWSMEDIWQLTQ\*  
MVDESSNADKRIHINQEAEVRKGWPWTMEEDLILINYIANHGEGVWNNLARSAGLKRTGKSCRLRWNLQYRDPVRRGNITPEEQLIMELH  
*Mol012057* ARWGNRWSKIAQLPGRTDNEIKNYWRTRIQQKVNGDAPDYSSQMIIDEASTSHTSSIEEGMAQQSYPIHPNTNPEAYPPSCNSGELGEN  
FWSMEDFWPIQSDQSLNGD\*  
MVSHTSCCLKQKLRKGLWSPEEDEKLFNHIIRFGVGCVSSVPKRALQRCGKSCRLRWNLQYRDPDLKRGFSQSSEEDLIISLHEILGNRWSQI  
*Mol014116* ATHLPGRTDNEIKNFWSCLKKLRQNGIDPSTHKPLNEEQNEDKSHNLNDSNQMNSAMRPVFDPFPALDFQPGTVLNTYDQLQQPPLIP  
ASDSLNASENYFYGESSASCINWNC SIGAELNFSSDSSYYYSSFQMKS FQNP SDACLDIPQSEFGGDLL\*  
MGRPPCCDKAGIKKGWPWTPEEDIILVSYIQEHGPVNRLVPTNSGLMRC SKC RL RWNL QYR PG IKR GNF S HEEE III Q ALL GNR WAAI  
*Mol006363* ASYLPQRTDNDIKNYWNTHLKKKIKKYQASVGSYITSSDSAGSTSHERVLGGYGADEIRNSCSSNSHTLHSSSTYASSAENISRLLEGWM  
RSSPNQTLNDKKLQHQMKKESITFNSNSFIMNQLNFDVEVNSQLPLEGSVIAWDKTATDSVFEENKQFKMMTYDDNKLKTQSQQPAMSV  
LEKWLEENPGQMDAFLETMF\*  
MERQRKRMTLGDEVMVLLRAHNMTSENDGDTMLLKEQLESSSTDEGSCCGSSTTGGGRVTLKGPWT AEDALLISYVRKHGEGN  
WNAVQRHSGLLRCGKSCRLRWANHLRPHLKKGAFSPEEEQFIQMHSKMGNRWARMAALLPGRTDNEIKNYWNTRVKRRSRAGLPLYP  
PKLSLQTSNENQLIQSASELSSGNHQNIGVLQGTMNGTLEFRCHPHKANGPLSPPRFPDIPVTDLPCHGLEYYTRSFLNSGANHFKQTWE  
*Mol017152* SETFSPGCHVNQNSIMVPAFEELPSNSETVYLNTGLGYPYDPDPENKNLASFICSTPGNPGNFSSRLLPGAVKMELPSLQYPEADYIDWTSS  
SLLKSSYDAVDMYIQSPENVSVHSDCASPRNKGLL EDLVQESHAISSGKKQSFEKSF DRA VAAVMAS GTVKWEEIRDPTSPFCLSAVSLFN  
DCNPTIISTFDESSACETPMGDKQDKYTPNLPYFLRPVLLGSGWLMGNNSGDAEDSIAGALDENLHKERAPVPIPVPAGISSMASLEAYPWTN  
MPRVCQMSEH\*

MGRSPCCSKVGLHRGPWTAREDALLTSYVQNHGEGNWRSLPKLAGLLRCGKSCRLRWVNLYLRPDIKRGNIGPEEEDIIRLHRLGNRW  
*Mol016709* SLIAGRLPGRTDNEIKNYWNSHLSKKLKKQGLKLREATPRTKQSNSSSNNKKQSTKIINQSETLGGTNETKIYAPKPTRLTSRIHVMENSSEE  
EKGSSDEMELSANLYSDGGEHDFLNTQYLDLGFDQFLPLQQDSVMFERLYDEYSQLLQSEVNDVNLFAYDQYLMV\*  
MERNSCCFKEGINKGAWSSSTDLLAFVNAHGEVKWTTVPSKAGLKRSRKSCRLRWLNCLRPNVKRGNFSEEDDLIIRLHKLLGNRW  
*Mol023305* SLIAGRLPGRTDNEIKNYWSTTLSKKASFRHLIRQSSATRPPASNREIPTQSAEESTAKMVDEMPENSKGCGIVKEQQFQVEENMALNFG  
SFDDDTMVALRDQTLMEFNGPMDFENWMLNDEYVDYLPADQIQSLPSLFDIGGEF\*  
MVRAPCCEAMGLKKGPWTHEEDNILVSYILTNGHGNWRALPKAGLLRCGKSCRLRWVNLYLRPDVKRGDFSKEEEETIYMHAMLGNR  
*Mol011069* WSAIAAKLPGRKDNEIKNFWHTHLKKRNLPSQFIKKTPRTANPDEPKEEDKFEDQISPVFIQNESYFSENITESNSVDMKQNSIDSFEYFH  
DFDEILWSEEFTVTGEEEDGSIGLNFGKPSLSNEDSISFWLNLLAESGNLE\*  
MMGDQEEPNSVDKMINNSNEEAEVVRKGWPWTMEEDLILMNYIAIHGEGRWSNLARSAGLKRTGKSCRLRWVNLYLRPDVRRGNITPEEQL  
*Mol010957* LIMDLHSRWGNRWSKIARQLPGRTDNEIKNYWRTRIQQKVKDGETVCNSSQMMKYEGSSSHTGGLEEIAQTSYPIYPNANPQEAYVPTYS  
ESNPNEYLSAEDFWSIQSFNGL\*  
MEVQYGWGTFEDGWRKGWPWTPEEDKLLTEHVKLHGEGRWNCVSRLTGLKRSRKSCRLRWVNLYLRPDLKRGKITPHEETIILELHAKWG  
*Mol023320* NRWSTIARSLLGRTDNEIKNYWRTHFKKESTTKNIKRARAKFLKQQHQQLQLEVPQFEEIAITQLMEIAYMCNMPYVFQGEETRKSVM  
SSDNRLGDGEAYYATWENLWNLDDLGMDQAVFYY\*  
MGRAPCCDKANVKRGWPWSPEEDEALRSYIQNHGSGGNWIALPKKAGLKRCGKSCRLRWVNLYLRPDIKHGCFTKEEDDIIFTLYSKIGSRW  
*Mol007569* SVIASKLPGRTDNDVKNHWNTKLKKRMMETQARLSGSHYRSSAPPLMASEPLALTDSLASICASIRPTDQIESQSFNGSFDEPLDLRVPR  
QNPSFLDDFGSITDLLCSSTYEETIETIWADASEEIKLGELSQSVALEY\*  
MGRAPCCAQGLKKGPWTPEEDKILVDYIQSNHGWSCLPKLAGLLRCGKSCRLRWVNLYLRPDIKRGPFTEEQKTIQLHGIVGNKWST  
*Mol016869* IASQLPGRTDNEIKNYWNTLKKRLLRMGINPDTYAPASPSSAGGGGAGFPVTRHMAQWESARLEEARLSRESLLFSSASSAAAVSA  
DSEPADDSLPAARKPESDFFLRIWNSEIGDAFRKPLPSTLPRSAEEATTAPTEESKSCASAGGEAPSAPDSSSNELDETSRRTSST\*  
MGRHSCCHKQKLRKGLWSPEEDEKLLKHITKYGHGCVSSVPKLAGLQRCGKSCRLRWINYLRPDLKRGTFSQQEENLIELHAVLGNRW  
SQIAAQLPGRTDNEIKNLWNSCIKKLRQRGIDPNTHKSLSETENPDENKVSTSSERNSILYTGDSLKQTVPQLTSSLMQSVDKNSIPVKEFC  
*Mol018126* IDNATTCLRSSNSISSFPLPQLNYGTSATASLPLSSNPFLWFNQNCRVDMNPELSCTSMSTMGPSISSLVLTNSIDLKSPVNLSCLPPTCT  
GAPIFSYLDAGNPSRCSSGSSSSSSFDSGFLSWPDLTTEKEIQINFQGDPEELKWSEYLQGNFPVSSVLHSHNQPLYGGDANSESHFDIEGV  
GLWHQNQQPQHQHQQQQQASDLYGKEYQRISTLFGQI\*

Mol000176 MGRAPCCDKANVKKGWSPEEDAKLKSIEKHTGGNWIALPQKIGMKRCGKSCRLWLNLYRPNLKHGGFSEEDNIICSLYVTVGSR  
WSLIASHLPGRTDNDIKNHWNTLKKLLGKSRKDHQHHSRRIPKQLEPKSEETNDFWLDPALPPYPETDSQASIKVLMKLGRISID  
EEAEIPPLINAPDHNSIYCSSLMASSAQLSSNECLSTNLNIFASNEVKLEFDNYSLYGMTTMAEEITGLGMPEAVNWSTDVSSSI  
YSPMASTSVDVSYHGSMQQVYQDHQMHLGMELSFKEYE\*  
MKFYKRMGRHSCCYKQKLRKGLWSPEEDEKLLEHITKYGHGCWSSVPKLAGLQRCGKSCRLWINYLRLPDLKRGTFSQEEENLIELHGV  
LGNRWSQIAAQLPGRTDNEIKNLWNSCIKKLRQRGIDPNTHKPLAEIDEQREKIAEIDSSGHPTPEPAKQTEQPAETAVLNNFVRPANSSA  
Mol002856 ASYYSLPNLTYSDECGNIGNILQQFWFNQSSKFFNTINPNEFSFNSVSSLPSVPRSTLSTSKEKPLTNLLMENSPSGFYWEAGNSSSAS  
SGSNDPLFDGSIFPWTQLMPERDTNIQLHGETEDLKWKSEYLNGSIPLSTDLQSQNPELCNGVKVEEQFGIDGLSIWLQNHQQQQQQQQQQ  
QASNFYGKDCQKDMVC\*  
MGRAPCCEKVGLKKGRWTAEEDQLLVKYIKTNGEWSRSLPKAGLLRCGKSCRLWINYLREDLKRGNIKSEEEDIQLRANLGNRW  
SVIAGHLPGRTDNEIKNYWNSHLSKKVEGLHDKEDENCATGVTKVRKRKGGRPSKSAKKKAEVISSMDEGTKLKDVMASKSEQGE  
SIVTDLEPQELSLEDLPSIEILLVDEENIEGGRALNPNEEGKQKEDSGVIVEVLSNEEGSSFDEIEKLVDWELEELALRLWEEGEGVGEV  
TPWVWEDESPRINGEFGDFDYEKFDAFKEDDYLDDWLLSDASECSSWFSSCG\*  
MVRAPCCDKKGLKKGRWTVEEDETLMNYIAENGEGWSRSLPKAGLLRCGKSCRLWINYLRSIDLKRGSIKSEEDEIIKLHATIGNRW  
VIAAQLPGRTDNEIKNYWNSHLSRRVHCRRHGESKTFIYDIGSIPSPGKRRGGRTSRAAMMKNSSSMVSGSIREDQISPNPQNQVLNHT  
Mol008232 NNNLCISSLTEKENSSLTFDFDFLEEVLGPNGDIDAVSLEANEMGESRRATCSGEKEVELAMEEESGTMMEKMLKWDFESLEA  
KLWEEDGSDMWPLWDISGDIIFDDEEPLGSWLLA\*  
MGRAPCCDKENVVKKGWSPEEDVKLKSIEQYGTGGNWIALPQKVGLKRCGKSCRLWLNLYRPNLKHGAFSEEDNIICSLYIRIGSRW  
SLIAAQLPGRTDNDIKNYWNTKLKKLLGKSSHKNHHQSQYTRRAPKQDPNNLQEINTVEISNGSTSSASYWIQPATPTYMSSTEIKRFLP  
KLEGVPPLITPDHSDLNDNTNSYLLEASPQPSSFTNCLEDDIFGHFDSFYGSNGMSGEITGLLSMPDQVFNSLMYPPMAVSAKASYQG  
TIGANGGLV\*  
MGRAPCCSKVGLHRGPWTSREDALLTSYIKNHAGSWKSLPKRAGLLRCGKSCRLWMNYIRPDIKRGNIKSEEEDIIRLHSLLGNRWSL  
Mol019578 IAGRLPGRTDNEIKNYWNGHLSKKLRNQGFAMRAAVSRRPKPSRDHSSMKTNNTTEMKSTSEKATVSKIYAPKPRIERRYRNYVMSA  
VTESENEETEGSDGRLDSGEESSSENYQENISCSDNGEEANLLDVNRYLGLLDSENGDFFLQDHEVVERVYQEYLQLLNVETEKEKQII\*  
MGRAPCCSKVGLHRGPWTAREDSLLISYIQNHGEGNWRSLPKAGLLRCGKSCRLWMNYLRPDIKRGNIKGPQEEDIIRLHCLLGNRWS  
Mol011408 LIAGRLPGRTDNEIKNYWNSHLSKKLKQGFAIREETPRPKRTATPNYHNKKNNNNNSKLSETMQSDGAVENAKIYAPKPTRFKPTWSV

MEKSESVTEEYEKGSSDASSGTNYDVDLASWSHDDHGGEFDQAVGFHDATHLDFAADFFMQDESLQRLYDEYSQLLQLEVGANQLAEP  
LMQ\*

Mol005657 MGIRPPCCDKLNVKGLWTAEEDAKLLAYVSTHSGGNWTVPKKAGLKRCGKSCRLRWTNYLRPNLKHEGFSSQEDELIVTLHATIGSR  
WSIIANQLPGRTDNDVKNWNTKLSKKLALNGIDPVTHRPISEIKHSITLHFAAATAAGQPLPSAATVGVGHHDSRLISINRDLKKILLSP  
PIPPPLEPATPPVLWNASGQTAAAPRSFPPPPPPPPQDLEWVQFLAEDAFLCIDEHDAYRAPPATVDADFDFMEEEADVSSFIDEMLDRDR  
EIISEFSGLVGCHYAL\*

Mol020055 MMRRPETTNAASSKNGATVHKLRKGLWSPEEDDKLMTYMMTNGQGCWTDVARNAGLQRCGKSCRLRWINYLRPDLKRGAFSIEEEELI  
IHLHSILGNRWSQIAARLPGRTDNEIKNFWNSTIKKRLKNSSQSPSPPSHDKSPSDANKELIMEDIMFMRMNSSSSSSSMQAFSMTINY  
LFPFPDTVANDCFINDMSSLAHDHGMYNDGNAHGIAMDGGLKVEEGYDHFFVPP LDSASQEENGANLDYAYQNYSRNIGEINSNMMTL  
KDHDDETKNIKGSHFAGSHEKWEEGQESMRVGEWSLEDLIEDVSSFPLLDFQVE\*

Mol001669 MAWKKDSSKLNLSKSTPTLPLLQPQNLSQLKWFPSPLTLLPLTQLTSFPSRQTLRMKFWGKHNMVVAEEISRDGGGENTNDSSGQSK  
LCARGHWRPAEDSKLKEVAIYGPQNWLIAEKLEGRSVFYRKSCRLWFNQLDPRINRSAFTEEEEKLMAAHRLYGNKWAMIARLF  
GRTDNAVKNHWVHIMARKYREQSTAYRRRQLSQTMHLRKAIIFRSSRKTTFADHRDQERTDIFRQNDNEVQALQSSSYHQASILLTMHQ  
SAGHLPHNISVASSSSGETPAHSAEVEVNMDASHGHIERSISSSSPTDFLGSYLRE\*

Mol006740 MGRPPCCDKPGIKKGPWTPEEDLILISYIQEHGPGNWRSPINTDMTAASNVIAGLLRCSKSCRLRWTNYLRPGIKRGSFPTYEEGIIHLQA  
LLGNKWAAIASYLPQRTDNDIKNYWNTHLKKLKLQETIGSHNPLAIEATVNTEFAGVQLQQHPQYSSCTYASSTDNISRLLEGWMRS  
SEKNTMQSSSIDIKNSGDSLICHEEFYHEKLPEMMPVTAEA VVEVEQRSLTFLEKWLFDGTGHVDGFMLEPSDLQI\*

Mol000510 MPEEDEKLREMVT RGHPHNWNAIAEKRRGRSGKSCGLRFNQLDARIKRNTFKEEDEERLLSYHRIHGNRWAVIARLLPGRTDNAVKNH  
WHVIMARRSRETSEVLKLNQFIRSEEKQRREDLEIKFSEDIFCPNLRGGDETKS YGYNSIFQGQGHQFFSCYPNVHIFEDGIKEESSIEFYDFL  
QVNSSDSNATGKRSKMDEEEQEEHDKEKLESKGKVGPFDLVDSSHWDWST\*

Mol001948 MGRQPCCDKVGLKKGPWTTEEDKKLIN FILNNGQCCWRAVPKLAGLLRCGKSCRLRWTNYLRPDLKRGLLSESEEKLVIDLHSQ LGNRW  
SKIAANLPGRTDNEIKNHWNTHIKKKLRKGIDPLTHKPLPSEDQLPHQTQHCEIPYAVSDLSTAVPLRPLDSLEAFCTDDVPLM EPHEIIL  
PFTPSTTPCSSSSTTERTAWPSSSSSSSVKAEEIFPSMEWSEIYLWGMNDFMGWDFISHEGDGKLSSTDLFNQNQEPWKFELF\*

Mol002260 MGRQPCCDKLVKKGPWTAEEDKKVAFILNN GHCCWRAVPKLAGLLRCGKSCRLRWTNYLRPDLKRGLLTDAEEKIVIDLHASLGNR  
WSKIASKLPGRTDNEIKNHWNTHIKKKLLKGIDPVTHKLLNDQTSSTAMASPNSTVTDDEKFSKKHEPLDAEKVIINTVSQEESTNPQQN  
CSNAIDRDEQVIGCLWDDDMPFIDKLWSSPISNEAWERSSEWLLDYQEFGIGDLELGRVESIGFADEQIKLN\*

Mol023319 MTIIQDNSHQHMFQDASMPQHASTDGVLVPTPITALASQAISLYNRSHLDGWRKGPWTPQEDKLLTEHVKLHGEGRWNCVSRLTGLKRS  
GKSCRRLWVNVLRPDLKRGKITPHEETIILEHLAKWGNRWSIARSLPGRTDNEIKNYWRTHFKKGKTTNIERARAKFLKQQHQQLELE  
VPQFEEIAITQWEIAYMCNMPYVFQGEEFRKSIVSSDDIDWVMMRHIMPLGRIWNLDLGLDMGDQASFLLLEDGIGVKKTV\*  
MSTGKKQSPSIELVFLSLCMSIARAPCCDKANVKKGPWSPEEDAKLKSYIDEHGTGGNWIALPHKIGLKRCGKSCRLWNLRYRPNIKH  
GGFSEEDQIICNLFVSIGRSWSIIAAQLPGRTDNDIKNYWNTRLKKLLGRRRESSSTSQRHRLSDDKDCNTKPNGSTQILTASALERLQ  
LHMQIQGLHCPFSFYNNNTSLWPKLYPLKNDCFKQPLSTDATATSVHPLKLSQQAMEPIEQANISNSMHPNIQGSLGASSSSSNLDIELHDL  
LYGKESKLFSEIDSFNDLNIEEGTGWLGRNGFEKSSSSWDSAFAHPDSVLQEYGLGYDL\*  
MGRAPCCDKAIVKKGPWSPEEDAKLKAYIEEHTGNNWIALPKQIGLKRCGKSCRLWNLRYRPNIKHGGFSEEDRIICSLYVSIGRSWSI  
IAAQLPGRTDNDIKNYWNTRLKKLLGRRDLPPSQFSQLAPADQKLNDEGSNPNESSQNLTSAIERLKLHIQLQGLHSPFSYGNASL  
WPNNKLLQTLNSTDHISIATAASPLKHQQTNICNSMISNMQEHIVIPSSCNLEAELHNLLDGYKENYQFTQVDCLKEIMNDIDQKGFDW  
ESNEFVEKLSSTSWDSALQPDTVFIQDDELGYDQ\*  
MRPPTVVKKERASTTAVASGGAAAAPQQLLKKGPWTAAEADAILKEYVRKHGEGNWNALQKKSGLQRCGKSCRLWVNHFRLKES  
FSPEEETLIIRLHAQFGNKWAHMAKHLRGRTDNEIKNYWNTRVKQRKRAGLPLYPPEIQQHISSRCHGQVQNAWTANSPTLKPLQPTNS  
Mol006579 SFTSAMPLLSENPYGSILQDPSRGKNISFQFPFLTSPVLPENFDLGPPPLVKEELPSSQFSSNYGDEQMPHCNSGLLNDLLPESHGEEKLL  
SSTYLAIDLGLGYWDCPLGIKVIEEMLETDGRALIDMILTEMAMATPKTFVPDLYNNCSSSGSSGEFSNCPSSVTDEEIELDMPQLEWS  
YVHGTGGF\*  
MGRKPCCDKEGVKRLWTIEEDQRLVDFILNNGIQCWRVPKLAGLMRCGKSCRLWINYLRLPDLKRGALSEAEQQIQLHSNLGNRWS  
Mol005587 KIASHLPGRTDNEIKNIWNTRIKKKLKLQQSLDQITNNIEVERENHISKVEDKGLELEISTGSSKSSLFLELEQNWVQEKNIKQANVSISSSAS  
ASMDGNLNTSYWEGESNLHGGSNQLLWADTTDYFSSWDAYNCVDDFLRYENYP\*  
MEARKRDEFSSKRWSSEEDEILLKYIESHGLRNWIIGKNSGLSRDGKSCRLWNLHKPGLKKKLPFSKEEKFIIFSKHAALGNKWSKIA  
Mol016137 KQLPGRTDNEIKNFINTHMKKCLKTGTIPREISMKYAQGTGYGLPIASSDIADSVFQQWTELVDLPSIQNTEEDGKDIFLSSYLQNSQSSF  
ESLTQPQLAAPQQALITGFSTVLSSEQCSNLSISALLYSDYSMNTDLYSLLSKFI\*  
MHSGGGSGRKELPETAAAIRKGPMEEDEVLMDFVKKHGPRDWSSIRSKGLLRTGKSCRLWVNKLKDPLKTSQCKFSAEERIVIDL  
Mol002877 QARFGNWKARIATCLPGRTDNDVKNFWSTRQKRLARLLQTALPMSIKPFDDDHQAMIPFLQPIVTSCALLPYTLPCPDLIPFTEQYSNGQ  
CSHVVPYIEDPDSAKTLHMLNLDATALLIEPAIANSEICLQSSTPPQPPFDHSLLLEPLLPEGQDFIPEFGDMNFPFGCAENSHAMQLHMAP  
TFFDVGVGANDIKIEQPGTPESFFGDFPADMFDSLDDQPPPS\*

MEGQYYGWGTIDGWRKGPWTPQEDQLLIEHVKLHGEGRWNSVSWLTDEQILWSGLRSGKSSRLRWVNYLRPDLKRGKITAKEEAIIL  
*Mol017655* ELHARWGNRWSMIARSLPGRTDNEIKNYWRTHFKSTKNVEKARARYLRLQQDQKQQQLLSRSNIMKEETSSQTQMAMMPKEMEEEMTF  
LCNNMPLMLHEGGSSENQQPAVKIERAKRKLTTHGGAFGI\*  
MLGGVVRLGLGDFDCGACHVLLPVVLRFASFVWHLFLPGLISSLGLVYSRNAVSGGFYIFMSVKIMLGLTFRFLNMCSVEKDGDTKMPP  
EEQPDSSSNDEGSWSGSPTSGEGIALKKGPWTSTEDAMLIDFVKKHGEGNWNAVQRNTGLPRCGKSCRLRWANHLPDLKKGPLTREEE  
QFIIQMHAIGNKWARMAALSVFCNRNSYLSQCVTQLPGRTDNEIKNFWNTRTKRRQRAGLPSYPSNDCSGASNENLIQNAKLCHG  
*Mol016758* DIESSGVLQGSIYEMPRFPCTRPMSYAPLSDIHRTYMLSQUELRPYTRCFLNQGANHTKRNIIESEACLPGYHGSLGSVVSTFELPSEHSESMY  
QNLGLGYSYDPDPDNKNLISFGCISPGSHGSSHENLSASRCSSGTVKLELPSLQCPETNYSNWTAPPYHVDVPSPPENAPFLPDRASPRRNGL  
LEALVHESKTMNCGKKQSSEKSSCSSAITLSDMMESTAVNLCTEEWEETSQDQSPFSQSVERAPITSNSFDEFHPKDPLGSEATMAVEEAS  
ATSLPDKEPSHWPDFLRPDALLESNWILTD SHRVKETSDTSFELLGEDLCTAMVSLDSCPWN SMP SVCQIPEYL\*  
MAANDVDRIGKPWSPEEDEMLQMLVEHWSLISKSI PGRSGKSCRLWFNQLSPKVEHRPFTPDEDETIISAHRRFGNKWATIARLLSALITP  
*Mol028701* LSHWNSTLERKEAAAAAAAWTSEERMMGLWRIAGRSSGRMAPGSVSARVGKVIKADAPDSTTGKWNPCDPFTFLTLSLPGSSCGQNESS  
DNQKQTDPQLEKKPPSVSMASPFSLFLEALQEIIHQEVKNYMSGLEHRGILPPPLPPEEDSKLNSAKGIGISRIN\*  
MGRAPCCDKANVKRGWPWSPEEDAALRSYVERHGTGGNWISLPQKAGQLTYACILSFLFFKALNDAAKAAAFANYLRPDIKHGGFTEEE  
*Mol001134* DNIIFCLYKTIGSRWSVIASHLHGRTDNDVKNYWNTKLMKKIMAAGETINSPISNNQNTNKFHQPSPLLHHHQFKFRDWIQLVSTERRSS  
LTLQSSQWTSSITVDDGEGVTKPLPSSRSLVSPPGQLLGFTSGTYESPDSLWANTDTKPQGVYQSLYS\*  
MGRIPCCEKDNVKRGQWTPEEDNKLSSYIAQHGTRNWLIPKNAGALLDRWSLIAAQLSGRTDNDVKNHWNTKLKKLSGMGIDPVT  
HKPFSHLMAEATTAPPQVAHLAEALGCFKDEMHLTTKRRIDFSSTYAVGVYPTPVPPPSSGEPNLVSDINGEETIQKIKMGLSRAVMQ  
EPNPVKWGSTANGEPDNHNLMC E MYPMAIDQGYMYGDPSAYVNDGEGSTWSTCNGGGGSAAAQQHETGSRGYLLKGEEDDAE E S  
GVKGGSKEDAGVFGSECVLWDLSEDLMNHIV\*  
MGRAPCCDKASVKKGPWSPEEDERLKSYIEKHGTGGNWIALPHKIGNFYFYAGLFMILIWSIIAHLPGRTDNDIKNHWNTKLKTRLLGK  
*Mol012110* QRKNQQNRRSCNLQVMKKNKADNDQSASATTEANKAWLNLPISTITFHSTDHASYDNQSQTISKLQMKLADVRLPCCNGPHQVQVA  
PSLRIPQAIYETPLNTMAYSSHENTLNDGSPLKNVGPEYFEQGFNYSNNNSLMKLEGFDFFYGMSSFINESINVSESITWSEMNSFTSVLPIS  
STSEETLDFTSWETVKQC\*

Mol018336 MGRAPCCDNMGVRRGPWTPEEDQILISHIQRYGHGNWRAIPKQAAGKLPGRTDNEIKNLWHGHLKKRFDPNQNMKEAKQKNRGNSKAK  
EFKQATLEENVSSACSTTNDRDISSSVISTVGGENNSKTNMNYQLLQFDDSLCCFEPQSITKNCSKLIFITDDFNPMFSYNGEGSNFWNM  
LGKAANLQDWQNM\*

Mol018337 MGLERPWTPEEDQILISHIQRYGHGNWRAIPKQAGLVRCGKSCRLWENHLRPGIKRGNFTKEEMDAVISLHAVLSSRHVFFSLHYCQWS  
AIAGKLPGRTDNEIKNLWHGHLKKRFDPNQNMKDAKQKNRGNSAKEFKQATLEENVSSACSTTNDRMSSSVISTVGGENNSKTNM  
YQLLQFDDSLCCFEPQSITKNCSLNEIFITDDFNPMFSYNGEGSNFWMNMLGKAANLQDWQNM\*

Mol013317 MHSGSSGGGVRCRSRKELQSTETAAIRKGPMMAEEDAVIDEYVKRYGPRDWSSIRSKGLLPTGKSCRLWLNKLRPDLKSGCKFSAEEE  
WVVIDLQARFGNWKARIATYLPGRTDNDVKNFWSTRQKRLARLLQTPLPVGSRRNQGVPMPPAECMFEPNCNSGDLPYNDPQCLDLIPF  
TAECANSKCIHPPFVEEPDAMKMVLMSLDLPLSLLKPAITDRELCLPSSSSAPQSPFDHSLPDPLLSEGQGLILEFGEMSSPGQFC  
QVMQLPPSSLLDLQFGDHGVKIEHPATPESFFGDFPADMFEFMDQPPVS\*

Mol012133 MTLSVQLKEKPAVKPPETSAVTGTTTEAPQSLKKGHWTAAEDAILKRYVEKYGEGNWNAVQKNLGLQRCGKSCRLWANHLRPNLKK  
GAFSPEEEALIVQLHAQLGNKWARMALQVLGLL\*

Mol021537 MAARCRDVDRIGPWSPEEDEMLQILVVKHGARNWSLISKSIPIGRSGKSCRLWCNQLSPTVEHRPFTPEEDRTIISAHQRFGNWKATIAR  
LLNGRTDNAIKNHWNSTLKRKYSGAALEDEGRSLKRSNSAGLSFSPGSPSSSDVSDSSHHSQPLMTPPPVA  
IDTDSSGTGSITISDPITSLSLPGSASDQSEASDHHLRQNQSDLLLALPTKPEKLPLAAA  
ETMIMSPSHESLCNTVIKRIGISKID\*

Mol011587 MGRLRVREEPSEAKRVICAALWRPLYVEKDQSLVMQKPMQGEAFPDAQVYYYQIEGGRADEMDCASVNGGKSIETSSSSVMESSIGA  
VRGQWTAEEDRMLIRLVKQHGIRKWSQIARIFTGRIGKQCRERWHNHLRDPDIKKDSWTEDEEILLVQAHKEIGNRWAEIAKRIPGRSENSIK  
NHWNATKRKQSSKKRLRMAFHGDTSTPKHTVLQGYIKSITSSLHEITPITSPSASHSRTSNEFQMULLKVPQPHDSKLASQMVEELLSVEK  
QEMRAFEKEEQDFLGCSDIEYVSQFLNTEESFPSPSSNVTSA  
SPIRSVGEMDLMEIYNWHLHLP\*

Mol003679 MDGGSNEPFSPFKQMAQKPSWGFGTVLSEEMETKEHGRLNSKLCVRGHWRPAEADKLKELVARYGPQNWLIAEKLDGRSGKSCRLW  
FNQLDPRINRKAFTEEEEERLLSAHKFYGNKWLISRLFPGRTDNAVKNQWHVMMARRQRELSACKRRKSSSSCFITSVKMEEKININS  
SSNECTSSRNHFHLSMFLNSYKFPGTSVLIGFDGKPEASAETVVAHEREKMSLPPIDFLGVGAT\*

MAADKPEESKLCPRGHWRPGEDDKLRQLVQEFGPQNWSIAEKLQGRSGKSCRLWFnQLDPRINRRPFTEVEERLLAHRFHGNKWA  
*Mol015625* LIARLFPGRTDNAVKNHWHVIMARRQREKTKFLIDKSSFQQNHSHSILNQQTCCSISPQFNHYKYNYGILQSSHQPLQMFSNSSNIYWRF  
GMLDGHMGCCRTVSGGVNQEEDNDEALRSKNVYIDFLGVGKD\*  
MENLDAVKHGEMKACPRGHWRPREDEKLRLVVEFGPQNWTISEKLQGRSGKSCRLWFnQLNPRINRRPFTEEEEESLLTAHKIHGNK  
*Mol023861* WALIARLFPGRTDNAVKNHWHVIMARRQREKAKFLCKNGPSSTWPafSNFSLTSERRVNYGILESSRFLNVPLLFCDAYPACSLSGTGGS  
GMIRNMNEVRLRGCSNSREILSINCRRGIQFLEEGNDEASWRREDLTYIDFLGVGKDC\*  
MSSDHAAAPAPAPAPSTQAKKDRHMVSWTQEEDDLLRAQVALHGSDNWTIVAAQFKDKTGRQCRRWLTYLNTECKGGWSQEEDML  
LCEAQKIFGNRWTEIAKVTGRTDNAVKNRFSTLRKKRAKHHTSDENNNSCLHPSNKKIMIEPSANKQQNRYGDSSYVNSHESLTSTH  
*Mol017683* DITGTQSRPPLAVLTKNFNNLSCVQAHCHLDSNTKLTACDKMHHLPLKQLQIVRSRAISLEGMIQNYCFATRELLSSLAVKACSENRNQSS  
EDAWKSYMIWTREGGSSLSSFSEMDFLLDNFEGVFEDFQCGDTEIQLSTRVVVDLENSQTSSISTGCTHDDPRNNVDKHQLNHCSVGCNEGE  
SHQHEGISAPVKVCQGGTMSPSLELTQNRENLLVSSKSEFDSPKTIPPFSFTEEIPSPEFSSVSFDL\*  
MKERQRWRAEEDAILRAYVKQYGPREWNLVSQRMNVGLERDAKSCLERWKNYLKPGIKKGSLTEEEQRLVIHLQSKHGNKWWKIAAEV  
PGRTAKRLGKWWEVFKEKQQRELKESNKISSTPIEPGKYDRILESFAEKLVKQRPVTPLMASPLLPWLASSNNTSSPSVALSLSPSTLTAA  
PPTPWVQIERGPENTLGLVNAQQNVTNSQQNLLGELVECCREIEGRKEKIEEIESKVRELREEQKLALERIEAECWEQLLVVRRDAESKE  
QKLAELWSAKHAALSKLIRQMTGHH\*  
*Mol006728* MGLSLASPPSLFCSFENNGRINESGVILLEQQDGFFCGGKGGSFVVEKNIHNMELEKRENETRLSKLCRGHWRPAEDAKLRKLVALYGPQN  
WNIISEKLDGRSGKSCRLWFnQLDPRINRNAFTKEEQKLLSAHKFYGNKWALIARLLP\*  
*Mol009335* MDREWRKGKGAAWTREEDAKLTELCEAHDKRNWTVISSEIPGRSVAACQRWINHLKPAIEHPPFTDEENAIIVGANQEQRKKWERIARL  
LPGRTANAIRYHWKMNLCHLRNAPGSSQQAENL\*

---

**TABLE S2.** Ka/Ks analysis of *CsMYB* genes

Subgroups	Gene pairs		Ka	Ks	Ka/Ks	Divergence time (mya)	Purify selection
S1	<i>Mol017692</i>	<i>Mol005176</i>	0.27	1.77	0.15	97.35	Yes
S1	<i>Mol018189</i>	<i>Mol017692</i>	0.16	1.46	0.11	80.19	Yes
S2	<i>Mol018337</i>	<i>Mol018336</i>	0.02	0.02	0.82	1.30	Yes
S2	<i>Mol011069</i>	<i>Mol018337</i>	0.43	1.06	0.40	58.51	Yes
S2	<i>Mol020712</i>	<i>Mol015023</i>	0.29	1.18	0.24	64.61	Yes
S3	<i>Mol010269</i>	<i>Mol010337</i>	0.35	1.91	0.18	104.97	Yes
S4	<i>Mol003893</i>	<i>Mol008437</i>	0.26	NaN	NaN	/	/
S4	<i>Mol008698</i>	<i>Mol009531</i>	0.18	1.35	0.14	73.96	Yes
S4	<i>Mol008437</i>	<i>Mol000543</i>	0.26	2.03	0.13	111.32	Yes
S4	<i>Mol004081</i>	<i>Mol019958</i>	0.22	1.92	0.11	105.70	Yes
S5	<i>Mol023305</i>	<i>Mol012178</i>	0.49	NaN	NaN	/	/
S6	<i>Mol011449</i>	<i>Mol028264</i>	0.04	0.05	0.66	3.00	Yes
S10	<i>Mol010343</i>	<i>Mol001350</i>	0.24	0.97	0.25	53.36	Yes
S11	<i>Mol013646</i>	<i>Mol008801</i>	0.05	0.13	0.37	7.08	Yes
S11	<i>Mol008801</i>	<i>Mol008800</i>	0.16	0.53	0.30	29.17	Yes
S13	<i>Mol002856</i>	<i>Mol018126</i>	0.34	3.26	0.10	178.98	Yes
S14	<i>Mol013852</i>	<i>Mol001734</i>	0.19	1.01	0.18	55.54	Yes
S14	<i>Mol019578</i>	<i>Mol000176</i>	0.24	1.48	0.16	81.28	Yes
S17	<i>Mol023320</i>	<i>Mol023319</i>	0.11	0.09	1.15	5.17	No
S17	<i>Mol021224</i>	<i>Mol019840</i>	0.23	0.96	0.24	52.84	Yes
S17	<i>Mol023319</i>	<i>Mol017655</i>	0.24	1.15	0.21	63.16	Yes
S18	<i>Mol012133</i>	<i>Mol006579</i>	0.23	NaN	NaN	/	/
S18	<i>Mol017152</i>	<i>Mol016758</i>	0.35	0.86	0.41	47.26	Yes
S18	<i>Mol012137</i>	<i>Mol012133</i>	0.12	0.37	0.31	20.40	Yes

S19	<i>Mol010957</i>	<i>Mol012057</i>	0.16	1.06	0.15	58.45	Yes
S20	<i>Mol002558</i>	<i>Mol007990</i>	0.22	1.22	0.18	67.16	Yes
S21	<i>Mol003679</i>	<i>Mol022732</i>	0.32	0.98	0.32	53.86	Yes
S21	<i>Mol011788</i>	<i>Mol000510</i>	0.28	1.09	0.26	59.85	Yes
S21	<i>Mol028471</i>	<i>Mol001669</i>	0.28	1.16	0.24	63.88	Yes
S21	<i>Mol000510</i>	<i>Mol018713</i>	0.36	2.11	0.17	115.89	Yes
S21	<i>Mol023861</i>	<i>Mol015625</i>	0.22	1.70	0.13	93.44	Yes
S22	<i>Mol028701</i>	<i>Mol013522</i>	0.06	0.12	0.55	6.42	Yes
S22	<i>Mol013522</i>	<i>Mol021537</i>	0.26	1.31	0.20	72.23	Yes
	<i>Mol002877</i>	<i>Mol013317</i>	0.20	0.70	0.29	38.70	Yes
	<i>Mol016709</i>	<i>Mol000639</i>	0.32	1.22	0.26	66.77	Yes
	<i>Mol010990</i>	<i>Mol016869</i>	0.45	NaN	NaN	/	/

**TABLE S3.** Protein secondary structure prediction of *DrMYBs* and *CsMYBs*.

Subgroups	Gene ID	Alpha helix (%)	Extended strand (%)	Beta turn (%)	Random coil (%)
S1	<i>AtMYB96</i>	29.26	5.4	2.56	62.78
S1	<i>Mol005176</i>	29.39	6.07	2.88	61.66
S1	<i>Mol017692</i>	32.33	4.67	3.33	59.67
S1	<i>Mol018189</i>	35.03	6.05	4.14	54.78
S1	<i>OsMYB60</i>	36.98	6.43	2.89	53.7
S1	<i>AtMYB60</i>	39.64	5.71	2.5	52.14
S1	<i>Mol006363</i>	37.54	6.83	4.1	51.54
S1	<i>Mol006740</i>	42.75	4.58	4.2	48.47
S2	<i>Mol018337</i>	30.71	4.56	4.15	60.58
S2	<i>Mol020712</i>	32.34	4.26	5.11	58.3
S2	<i>Mol013321</i>	35.62	3.86	5.58	54.94
S2	<i>OsMYB4</i>	35.41	4.67	5.06	54.86
S2	<i>Mol011069</i>	35.78	5.6	4.74	53.88
S2	<i>Mol015023</i>	37.96	3.67	4.9	53.47
S2	<i>Mol018336</i>	41.45	3.63	3.63	51.3
S3	<i>Mol010269</i>	38.87	9.43	4.53	47.17
S3	<i>Mol001517</i>	35.79	13.11	5.74	45.36
S3	<i>Mol010337</i>	43.45	8.61	5.62	42.32
S4	<i>Mol003893</i>	30.25	7.56	5.88	56.3
S4	<i>Mol008437</i>	31.34	5.07	7.37	56.22
S4	<i>Mol008698</i>	32.06	7.25	7.25	53.44
S4	<i>Mol019958</i>	29.72	8.96	8.49	52.83
S4	<i>Mol009531</i>	36.7	4.59	7.34	51.38
S4	<i>Mol004081</i>	34.66	11.16	5.18	49

S4	<i>Mol000543</i>	32.27	12.75	6.77	48.21
S5	<i>Mol023305</i>	36.71	2.53	8.02	52.74
S5	<i>Mol012178</i>	42.58	12.11	7.81	37.5
S6	<i>Mol011449</i>	43.12	2.29	7.34	47.25
S6	<i>Mol028264</i>	45.26	9.91	4.31	40.52
S7	<i>Mol008232</i>	40.72	14.66	5.54	39.09
S7	<i>Mol008979</i>	41.05	13.89	11.11	33.95
S8	<i>Mol001948</i>	29.74	6.32	4.09	59.85
S8	<i>Mol002260</i>	36.25	4.78	3.98	54.98
S8	<i>Mol005587</i>	43.04	7.17	5.91	43.88
S9	<i>Mol010990</i>	30.81	9.52	3.08	56.58
S9	<i>Mol016869</i>	36.3	7.78	5.56	50.37
S10	<i>Mol001512</i>	43.08	4.31	4.62	48
S10	<i>Mol010343</i>	39.58	12.39	3.93	44.11
S10	<i>Mol001350</i>	42.55	11.38	5.15	40.92
S11	<i>Mol008800</i>	33.76	6.11	4.5	55.63
S11	<i>Mol008801</i>	41.88	4.87	5.84	47.4
S11	<i>Mol013646</i>	35.11	7.63	11.45	45.8
S13	<i>Mol018126</i>	24.88	4.88	4.39	65.85
S13	<i>Mol002856</i>	29.5	6.27	5.74	58.49
S13	<i>Mol014116</i>	35.57	6.72	8.7	49.01
S14	<i>Mol014101</i>	33.68	8.59	3.09	54.64
S14	<i>Mol013852</i>	35.99	6.78	3.24	53.98
S14	<i>Mol007569</i>	34.48	7.76	3.88	53.88
S14	<i>Mol001134</i>	31.75	11.51	5.56	51.19
S14	<i>Mol001734</i>	39.61	6.17	4.22	50

S14	<i>Mol000176</i>	38.83	9.39	3.24	48.54
S14	<i>Mol019578</i>	37.19	9.12	5.26	48.42
S14	<i>Mol004798</i>	28.62	17.39	8.7	45.29
S17	<i>Mol019840</i>	36.96	7.83	6.52	48.7
S17	<i>Mol026352</i>	36.94	8.28	7.64	47.13
S17	<i>Mol023318</i>	32.52	14.63	12.2	40.65
S17	<i>Mol021224</i>	34.43	16.39	10.16	39.02
S17	<i>Mol023319</i>	44.32	10.98	6.82	37.88
S17	<i>Mol023320</i>	46.05	8.37	7.91	37.67
S17	<i>Mol006174</i>	50.89	7.14	5.36	36.61
S17	<i>Mol017655</i>	44.95	13.76	8.72	32.57
S18	<i>Mol017152</i>	22.74	6.32	3.79	67.15
S18	<i>AtMYB33</i>	25.38	4.81	3.65	66.15
S18	<i>Mol014836</i>	28.31	5.03	2.05	64.62
S18	<i>AtMYB101</i>	28.16	4.9	4.69	62.24
S18	<i>Mol016758</i>	26.25	9.34	3.54	60.87
S18	<i>Mol012137</i>	38.4	3.99	4.49	53.12
S18	<i>Mol006579</i>	33.6	7.8	5.65	52.96
S18	<i>Mol012133</i>	45.08	9.84	8.2	36.89
S19	<i>Mol012057</i>	38	4.5	4.5	53
S19	<i>Mol010957</i>	31.53	12.32	4.93	51.23
S20	<i>AtMYB2</i>	32.97	9.52	2.93	54.58
S20	<i>Mol007990</i>	34.66	6.86	3.97	54.51
S20	<i>TaPIMP1</i>	46.13	3.1	4.02	46.75
S20	<i>Mol002558</i>	43.48	5.53	5.93	45.06
S20	<i>Mol015419</i>	39.05	10.48	10	40.48

S20	<i>OsMYB2</i>	49.67	9.67	4.67	36
S21	<i>Mol014848</i>	22.72	11.24	7.49	58.55
S21	<i>Mol009191</i>	31.31	8.63	5.43	54.63
S21	<i>Mol023861</i>	35.15	5.86	4.6	54.39
S21	<i>Mol011788</i>	31.78	9.75	4.66	53.81
S21	<i>Mol000510</i>	32.19	11.16	4.29	52.36
S21	<i>Mol003679</i>	35.8	8.64	6.17	49.38
S21	<i>Mol015625</i>	41.78	4.89	4.44	48.89
S21	<i>Mol022732</i>	37.3	13.18	4.5	45.02
S21	<i>Mol018713</i>	38.59	12.86	4.15	44.4
S21	<i>Mol001669</i>	39.88	11.35	5.52	43.25
S21	<i>Mol028471</i>	42.74	10.26	8.97	38.03
S21	<i>Mol006728</i>	38.67	16.67	11.33	33.33
S22	<i>Mol021537</i>	26.07	7.26	3.63	63.04
S22	<i>AtMYB44</i>	21.97	10.82	4.92	62.3
S22	<i>TaMYB70</i>	23.95	9.28	5.69	61.08
S22	<i>Mol013522</i>	32.76	6.21	3.79	57.24
S22	<i>Mol028701</i>	35.66	5.81	3.1	55.43
S22	<i>Mol017415</i>	30.99	10.74	6.2	52.07
S22	<i>Mol009335</i>	49.59	8.13	7.32	34.96
S23	<i>Mol016109</i>	23.94	6.91	3.72	65.43
S24	<i>Mol003923</i>	33.45	3.45	4.48	58.62
S25	<i>Mol011587</i>	39.85	6.94	3.34	49.87
S25	<i>Mol001031</i>	41.91	9.25	2.89	45.95
	<i>Mol002877</i>	28.25	4.44	3.81	63.49
	<i>Mol013317</i>	27.24	6.81	4.95	60.99

<i>Mol000639</i>	24.07	11.11	6.67	58.15
<i>Mol011408</i>	29.78	6.25	5.88	58.09
<i>Mol020055</i>	29.23	8.62	5.23	56.92
<i>Mol017976</i>	34.7	4.1	5.05	56.15
<i>Mol004182</i>	31.01	8.54	5.06	55.38
<i>Mol017683</i>	34.65	8.84	5.12	51.4
<i>Mol012110</i>	36.24	6.38	6.38	51.01
<i>Mol006542</i>	31.07	11	7.12	50.81
<i>Mol016709</i>	37.98	6.59	9.69	45.74
<i>Mol005657</i>	43.64	4.81	5.84	45.7
<i>Mol016137</i>	39	9.96	6.22	44.81
<i>Mol011807</i>	57.05	8.72	3.36	30.87

**TABLE S4a.** Putative *cis*-acting elements identified in the promoter regions of *CsMYB* genes

	Cis-acting elements	Number	Function
Light responsive	3-AF1 binding site	7	light responsive element
	ACE	10	cis-acting element involved in light responsiveness
	AE-box	26	part of a module for light response
	AT1-motif	12	part of a light responsive module
	ATCT-motif	30	part of a conserved DNA module involved in light responsiveness
	Box 4	441	part of a conserved DNA module involved in light responsiveness
	chs-CMA1a	22	part of a light responsive element
	chs-CMA2a	9	part of a light responsive element
	GA-motif	30	part of a light responsive element
	Gap-box	10	part of a light responsive element
	GATA-motif	72	part of a light responsive element
	G-box	176	cis-acting regulatory element involved in light responsiveness
	GT1-motif	102	light responsive element
	I-box	35	part of a light responsive element
Hormone	LAMP-element	16	part of a light responsive element
	MRE	40	MYB binding site involved in light responsiveness
	Sp1	23	light responsive element
	TCCC-motif	41	part of a light responsive element
	TCT-motif	91	part of a light responsive element
	ABRE	151	cis-acting element involved in the abscisic acid responsiveness
	AuxRR-core	13	cis-acting regulatory element involved in auxin responsiveness
	CGTCA-motif	151	cis-acting regulatory element involved in the MeJA-responsiveness
	GARE-motif	14	gibberellin-responsive element

	P-box	19	gibberellin-responsive element
	TATC-box	20	cis-acting element involved in gibberellin-responsiveness
	TCA-element	58	cis-acting element involved in salicylic acid responsiveness
	TGACG-motif	151	cis-acting regulatory element involved in the MeJA-responsiveness
	TGA-element	31	auxin-responsive element
Abiotic/biotic stress	ARE	163	cis-acting regulatory element essential for the anaerobic induction
	GC-motif	7	enhancer-like element involved in anoxic specific inducibility
	LTR	39	cis-acting element involved in low-temperature responsiveness
	MBS	48	MYB binding site involved in drought-inducibility
	TC-rich repeats	40	cis-acting element involved in defense and stress responsiveness
Development	CAT-box	52	cis-acting regulatory element related to meristem expression
	circadian	31	cis-acting regulatory element involved in circadian control
	GCN4_motif	23	cis-regulatory element involved in endosperm expression
	O2-site	49	cis-acting regulatory element involved in zein metabolism regulation
	RY-element	12	cis-acting regulatory element involved in seed-specific regulation

**TABLE S4b.** The number (No.) of MBS elements in *CsMYBs* and 11 *DsMYBs*.

Subgroups	Gene ID	No. of MBS elements	Subgroups	Gene ID	No. of MBS elements
S1	<i>OsMYB60</i>	1	S14	<i>Mol019578</i>	1
S1	<i>AtMYB96</i>	1	S14	<i>Mol000176</i>	
S1	<i>Mol006740</i>		S14	<i>Mol004798</i>	
S1	<i>AtMYB60</i>		S14	<i>Mol014101</i>	
S1	<i>Mol006363</i>		S14	<i>Mol013852</i>	
S1	<i>Mol018189</i>		S14	<i>Mol001734</i>	
S1	<i>Mol017692</i>		S14	<i>Mol007569</i>	
S1	<i>Mol005176</i>		S14	<i>Mol001134</i>	
S2	<i>Mol015023</i>	1	S17	<i>Mol006174</i>	1
S2	<i>Mol011069</i>		S17	<i>Mol021224</i>	1
S2	<i>Mol013321</i>		S17	<i>Mol023318</i>	
S2	<i>Mol018337</i>		S17	<i>Mol023320</i>	
S2	<i>Mol018336</i>		S17	<i>Mol023319</i>	
S2	<i>Mol020712</i>		S17	<i>Mol017655</i>	
S2	<i>OsMYB4</i>		S17	<i>Mol026352</i>	
S3	<i>Mol001517</i>		S17	<i>Mol019840</i>	
S3	<i>Mol010269</i>		S18	<i>AtMYB101</i>	1
S3	<i>Mol010337</i>		S18	<i>Mol017152</i>	1
S4	<i>Mol003893</i>	2	S18	<i>Mol016758</i>	1
S4	<i>Mol008437</i>	2	S18	<i>Mol014836</i>	1
S4	<i>Mol000543</i>	2	S18	<i>Mol012137</i>	
S4	<i>Mol004081</i>	1	S18	<i>Mol012133</i>	
S4	<i>Mol008698</i>		S18	<i>Mol006579</i>	
S4	<i>Mol009531</i>		S18	<i>AtMYB33</i>	
S4	<i>Mol019958</i>		S19	<i>Mol010957</i>	
S5	<i>Mol012178</i>	1	S19	<i>Mol012057</i>	
S5	<i>Mol023305</i>		S20	<i>Mol015419</i>	3
S6	<i>Mol011449</i>	2	S20	<i>AtMYB2</i>	1
S6	<i>Mol028264</i>		S20	<i>TaPIMP1</i>	1
S7	<i>Mol008232</i>	2	S20	<i>OsMYB2</i>	1
S7	<i>Mol008979</i>		S20	<i>Mol002558</i>	
S8	<i>Mol001948</i>	1	S20	<i>Mol007990</i>	
S8	<i>Mol002260</i>	1	S21	<i>Mol006728</i>	1
S8	<i>Mol005587</i>		S21	<i>Mol028471</i>	1
S9	<i>Mol010990</i>		S21	<i>Mol001669</i>	1
S9	<i>Mol016869</i>		S21	<i>Mol011788</i>	1
S10	<i>Mol001512</i>		S21	<i>Mol000510</i>	1
S10	<i>Mol010343</i>		S21	<i>Mol018713</i>	1
S10	<i>Mol001350</i>		S21	<i>Mol003679</i>	
S11	<i>Mol008800</i>	2	S21	<i>Mol014848</i>	

S11	<i>Mol008801</i>	1	S21	<i>Mol022732</i>
S11	<i>Mol013646</i>		S21	<i>Mol009191</i>
S13	<i>Mol002856</i>		S21	<i>Mol015625</i>
S13	<i>Mol018126</i>		S21	<i>Mol023861</i>
S13	<i>Mol014116</i>		S22	<i>TaMYB70</i> 2
S10	<i>Mol001512</i>		S22	<i>Mol017415</i> 2
S10	<i>Mol010343</i>		S22	<i>Mol009335</i> 2
S10	<i>Mol001350</i>		S22	<i>Mol021537</i> 1
S11	<i>Mol008800</i>	2	S22	<i>AtMYB44</i> 1
S11	<i>Mol008801</i>	1	S22	<i>Mol028701</i>
S11	<i>Mol013646</i>		S22	<i>Mol013522</i>
S13	<i>Mol002856</i>		S23	<i>Mol016109</i> 1
S13	<i>Mol018126</i>		S24	<i>Mol003923</i>
S13	<i>Mol014116</i>		S25	<i>Mol001031</i> 1
S10	<i>Mol001512</i>		S25	<i>Mol011587</i>
S10	<i>Mol010343</i>			<i>Mol006542</i> 3
S10	<i>Mol001350</i>			<i>Mol002877</i> 2
S11	<i>Mol008800</i>	2		<i>Mol000639</i> 1
S11	<i>Mol008801</i>	1		<i>Mol011807</i> 1
S11	<i>Mol013646</i>			<i>Mol016137</i> 1
S13	<i>Mol002856</i>			<i>Mol017976</i>
S13	<i>Mol018126</i>			<i>Mol004182</i>
S13	<i>Mol014116</i>			<i>Mol020055</i>
	<i>Mol005657</i>			<i>Mol016709</i>
	<i>Mol012110</i>			<i>Mol017683</i>
	<i>Mol011408</i>			<i>Mol013317</i>

**TABLE S5a.** Expression profiles of *CsMYB* genes in leaves

Genes	L1	L2	L3
<i>Mol009531</i>	150.12	149.09	86.66
<i>Mol008698</i>	86.98	199.03	95.21
<i>Mol001948</i>	69.57	153.43	11.58
<i>Mol002260</i>	67.15	287.74	7.18
<i>Mol019958</i>	54.06	56.99	16
<i>Mol018189</i>	43.79	14.21	38.25
<i>Mol020055</i>	43.34	95.69	0.97
<i>Mol005176</i>	42.44	64.78	36.82
<i>Mol021537</i>	32.64	91.16	72.31
<i>Mol018713</i>	29.75	39.38	0.25
<i>Mol006579</i>	28.57	26.32	22.59
<i>Mol001517</i>	24.85	87.73	0.39
<i>Mol021224</i>	21.33	21.15	37.37
<i>Mol017415</i>	16.97	8.86	5.5
<i>Mol017655</i>	16.48	58.32	70.31
<i>Mol010269</i>	15.67	100.92	4.6
<i>Mol004182</i>	13.31	14.47	0.09
<i>Mol011788</i>	11.97	20.69	5.33
<i>Mol016109</i>	10.75	13.54	11.94
<i>Mol003893</i>	10.55	12.86	9.82
<i>Mol004081</i>	10.26	10.27	2.03
<i>Mol007990</i>	9.34	60.4	57.12
<i>Mol008437</i>	8.31	14.41	4.56
<i>Mol002856</i>	7.92	2.56	3.17
<i>Mol007569</i>	7.39	7.23	3.55
<i>Mol016869</i>	6.94	2.08	10.65
<i>Mol026352</i>	5.51	10.45	3.63
<i>Mol000176</i>	4.39	31.66	5.16
<i>Mol016709</i>	2.72	7.86	1.74
<i>Mol010337</i>	1.81	10.42	0.44
<i>Mol015419</i>	1.52	89.42	57.79
<i>Mol011408</i>	1.11	10.41	5.66
<i>Mol004798</i>	0.22	9.59	2.64
<i>Mol011449</i>	0.15	5.15	0
<i>Mol015023</i>	0	5.9	3.7

**TABLE S5b.** Expression profiles of *CsMYB* genes in roots

Genes	R1	R2	R3
<i>Mol001948</i>	146.64	1.74	3.12
<i>Mol008698</i>	144.73	63.48	28.87
<i>Mol015419</i>	118.33	42.14	7.82
<i>Mol007990</i>	94.86	26.08	8.38
<i>Mol003923</i>	91.85	44.66	24.89
<i>Mol001517</i>	86.75	9.61	7.51
<i>Mol009531</i>	80.04	38.69	16.39
<i>Mol019840</i>	68.84	38.74	11.72
<i>Mol006174</i>	66.79	120.33	4.01
<i>Mol002856</i>	58.53	29.27	9.72
<i>Mol021537</i>	51.7	134.36	787.3
<i>Mol010269</i>	51.23	41.04	9.06
<i>Mol013852</i>	45.72	8.95	5.4
<i>Mol023318</i>	38.09	64.81	3.39
<i>Mol011788</i>	36.9	5.4	5.29
<i>Mol002260</i>	35.33	22.27	11.93
<i>Mol004081</i>	35.33	18.87	9.29
<i>Mol026352</i>	35.31	22.63	1.1
<i>Mol020055</i>	35.29	0	0
<i>Mol017655</i>	32.04	3.13	7.29
<i>Mol006579</i>	31.25	83.86	125.33
<i>Mol019958</i>	30.19	54.59	25.29
<i>Mol003893</i>	30.02	101.56	112.83
<i>Mol021224</i>	27.47	48.53	44.98
<i>Mol005176</i>	26.68	28.25	25.01
<i>Mol011408</i>	25.71	6.29	7.42
<i>Mol008437</i>	25.2	5.71	5.09
<i>Mol004798</i>	21.12	5.2	3.13
<i>Mol001734</i>	18.92	4.35	1.98
<i>Mol017976</i>	15.68	4.59	7.64
<i>Mol016869</i>	14.91	16.15	18.54
<i>Mol019578</i>	14.43	62.68	35.12
<i>Mol000176</i>	13.74	3.15	1.57
<i>Mol016109</i>	13.28	25.57	19.75
<i>Mol014101</i>	13.2	18.11	9.17
<i>Mol018713</i>	10.21	1.06	1.85
<i>Mol016709</i>	9.91	1.22	3.04
<i>Mol007569</i>	9.85	39.58	32.44
<i>Mol001512</i>	9.66	1.95	1.95
<i>Mol010337</i>	9.16	0.94	1.63
<i>Mol000639</i>	6.57	0.23	0.69
<i>Mol015023</i>	5.8	0.39	0.26

<i>Mol010343</i>	4.29	5.19	3.45
<i>Mol018189</i>	3.54	5.61	12.65
<i>Mol008801</i>	2.92	8.41	9.67
<i>Mol013522</i>	2.81	7.42	15.57
<i>Mol023320</i>	1.86	7.39	0.75
<i>Mol011807</i>	1.25	3.43	5.93
<i>Mol010990</i>	0.85	8.94	4.17

**TABLE S6a.** The fold-changes of *CsMYB* genes in leaves of *C. sinense* under drought stress treatment

Subfamilies	Gene ID	Fold change of L2	Regulation	Fold change of L3	Regulation
S21	<i>Mol011788</i>	1.728487886		0.445279866	down
S21	<i>Mol018713</i>	1.323697479		0.008403361	down
S22	<i>Mol021537</i>	2.792892157	up	2.215379902	up
S22	<i>Mol017415</i>	0.52209782		0.324101355	down
S23	<i>Mol016109</i>	1.259534884		1.110697674	
S18	<i>Mol006579</i>	0.921246062		0.790689534	
S17	<i>Mol017655</i>	3.538834951	up	4.266383495	up
S17	<i>Mol021224</i>	0.991561181		1.751992499	
S17	<i>Mol026352</i>	1.896551724		0.658802178	
S20	<i>Mol015419</i>	58.82894737	up	38.01973684	up
S20	<i>Mol007990</i>	6.466809422	up	6.115631692	up
S13	<i>Mol002856</i>	0.323232323	down	0.400252525	down
	<i>Mol004182</i>	1.087152517		0.006761833	down
S16	<i>Mol011449</i>	34.33333333	up	0	
	<i>Mol020055</i>	2.207891094	up	0.022381172	down
S8	<i>Mol001948</i>	2.205404628	up	0.166451056	down
S8	<i>Mol002260</i>	4.285033507	up	0.106924795	down
S4	<i>Mol008698</i>	2.288227179	up	1.094619453	
S4	<i>Mol004081</i>	1.000974659		0.19785575	down
S4	<i>Mol009531</i>	0.993138822		0.577271516	
S4	<i>Mol019958</i>	1.054199038		0.295967444	down
S4	<i>Mol003893</i>	1.218957346		0.930805687	
S4	<i>Mol008437</i>	1.734055355		0.548736462	
S9	<i>Mol016869</i>	0.299711816	down	1.534582133	

	<i>Mol011408</i>	9.378378378	up	5.099099099	up
	<i>Mol016709</i>	2.889705882	up	0.639705882	
S14	<i>Mol000176</i>	7.211845103	up	1.175398633	
S14	<i>Mol004798</i>	43.59090909	up	12	up
S14	<i>Mol007569</i>	0.97834912		0.48037889	down
S1	<i>Mol018189</i>	0.324503311	down	0.873487098	
S1	<i>Mol005176</i>	1.526390198		0.867577757	
S3	<i>Mol010337</i>	5.756906077	up	0.243093923	down
S3	<i>Mol001517</i>	3.530382294	up	0.015694165	down
S3	<i>Mol010269</i>	6.440331844	up	0.293554563	down
S2	<i>Mol015023</i>	NaN		NaN	

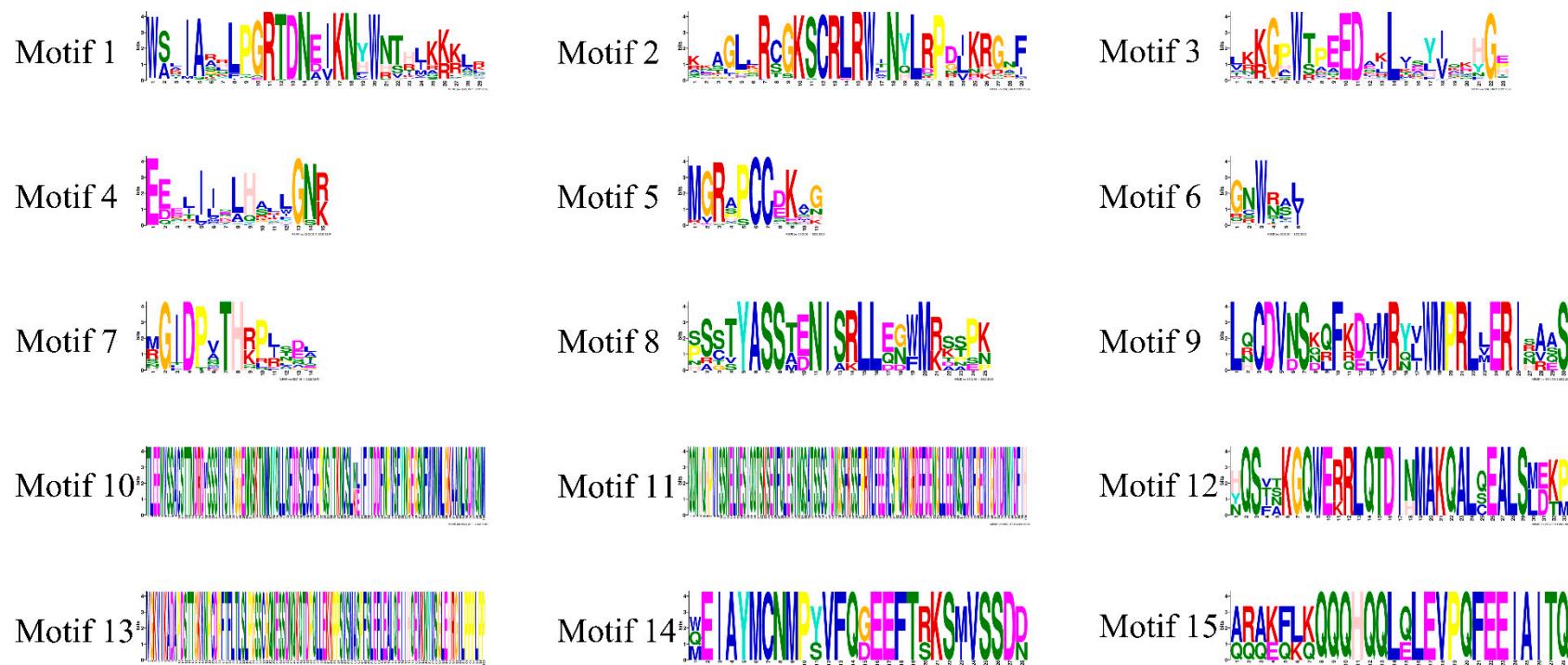
**TABLE S6b.** The fold-changes of *CsMYB* genes in roots of *C. sinense* under drought stress treatment

Subfamilies	Gene ID	R2/R1	Regulation	R3/R1	Regulation
S21	<i>Mol011788</i>	0.146341463	down	0.143360434	down
S21	<i>Mol018713</i>	0.103819785	down	0.181194907	down
S22	<i>Mol013522</i>	2.640569395	up	5.540925267	up
S22	<i>Mol021537</i>	2.598839458	up	15.22823985	up
S23	<i>Mol016109</i>	1.925451807		1.487198795	
	<i>Mol011807</i>	2.744	up	4.744	up
S18	<i>Mol006579</i>	2.68352	up	4.01056	up
S17	<i>Mol023320</i>	3.97311828	up	0.403225806	down
S17	<i>Mol006174</i>	1.801617009		0.060038928	down
S17	<i>Mol023318</i>	1.701496456		0.088999737	down
S17	<i>Mol017655</i>	0.097690387	down	0.22752809	down
S17	<i>Mol021224</i>	1.766654532		1.637422643	
S17	<i>Mol026352</i>	0.640894931		0.031152648	down
S17	<i>Mol019840</i>	0.562754213		0.170249855	down
S20	<i>Mol015419</i>	0.356122708	down	0.066086369	down
S20	<i>Mol007990</i>	0.274931478	down	0.088340713	down
S16	<i>Mol002856</i>	0.500085426		0.166068683	down
	<i>Mol017976</i>	0.292729592	down	0.487244898	down
	<i>Mol020055</i>	0		0	
S8	<i>Mol001948</i>	0.011865794	down	0.021276596	down
S8	<i>Mol002260</i>	0.630342485		0.337673365	down
S4	<i>Mol008698</i>	0.438609825	down	0.199474884	down
S4	<i>Mol004081</i>	0.534106991		0.262949335	down
S4	<i>Mol009531</i>	0.483383308	down	0.204772614	down

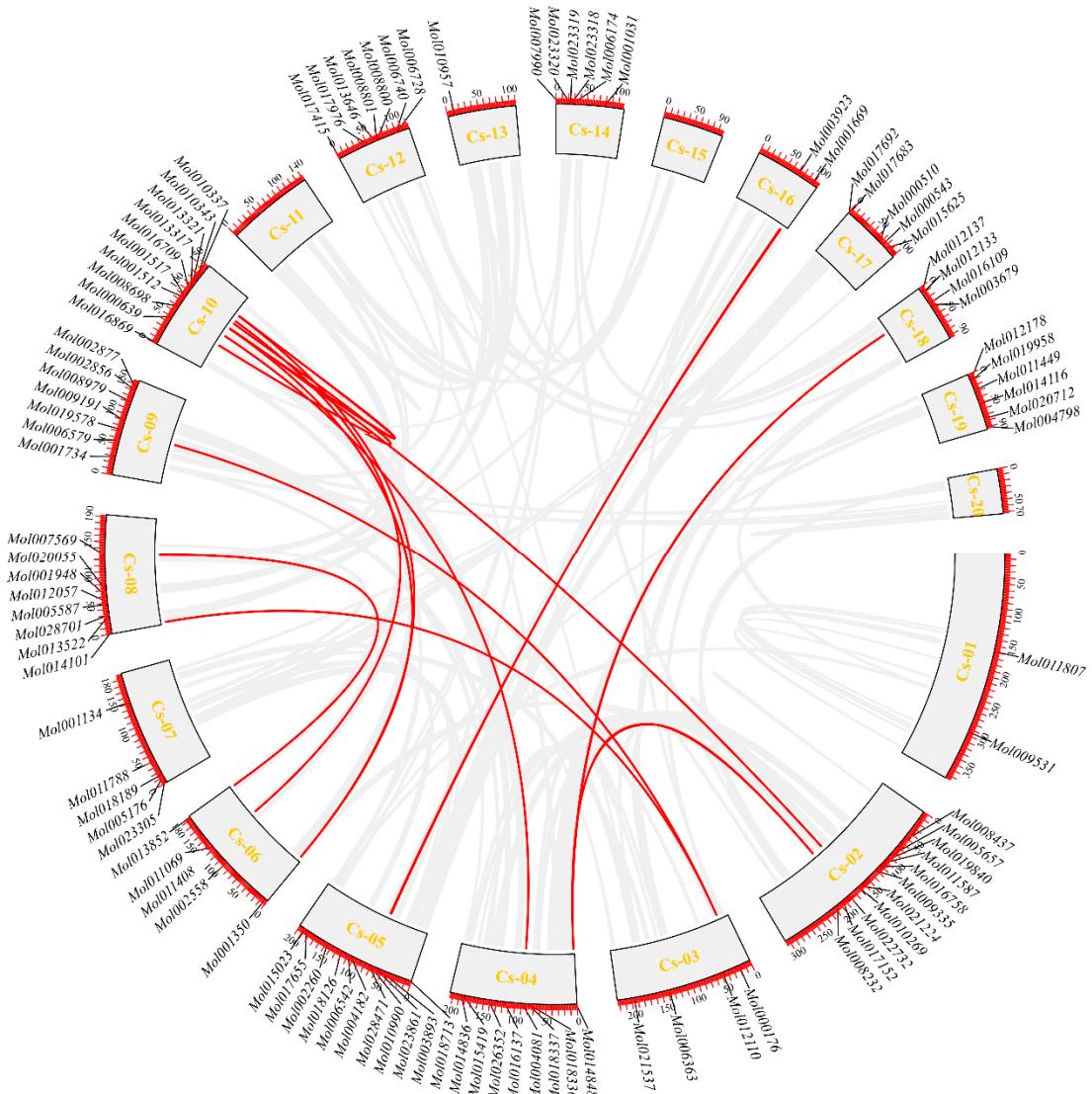
S4	<i>Mol019958</i>	1.808214641		0.837694601	
S4	<i>Mol003893</i>	3.383077948	up	3.758494337	up
S4	<i>Mol008437</i>	0.226587302	down	0.201984127	down
S11	<i>Mol008801</i>	2.880136986	up	3.311643836	up
S9	<i>Mol016869</i>	1.083165661		1.243460765	
S9	<i>Mol010990</i>	10.51764706	up	4.905882353	up
S10	<i>Mol010343</i>	1.20979021		0.804195804	
S10	<i>Mol001512</i>	0.201863354	down	0.201863354	down
S24	<i>Mol003923</i>	0.486227545	down	0.270985302	down
S14	<i>Mol011408</i>	0.244651886	down	0.288603656	down
S14	<i>Mol016709</i>	0.123107972	down	0.306760848	down
S14	<i>Mol000639</i>	0.03500761	down	0.105022831	down
S14	<i>Mol019578</i>	4.343728344	up	2.433818434	up
S14	<i>Mol000176</i>	0.229257642	down	0.11426492	down
S14	<i>Mol013852</i>	0.19575678	down	0.118110236	down
S14	<i>Mol001734</i>	0.229915433	down	0.104651163	down
S14	<i>Mol004798</i>	0.246212121	down	0.148200758	down
S14	<i>Mol014101</i>	1.371969697		0.69469697	
S14	<i>Mol007569</i>	4.018274112	up	3.293401015	up
S1	<i>Mol018189</i>	1.584745763		3.573446328	up
S1	<i>Mol005176</i>	1.058845577		0.937406297	
S3	<i>Mol010337</i>	0.102620087	down	0.177947598	down
S3	<i>Mol001517</i>	0.110778098	down	0.086570605	down
S3	<i>Mol010269</i>	0.80109311		0.176849502	down
S2	<i>Mol015023</i>	0.067241379	down	0.044827586	down

**TABLE S7.** The primers of *CsMYB* genes.

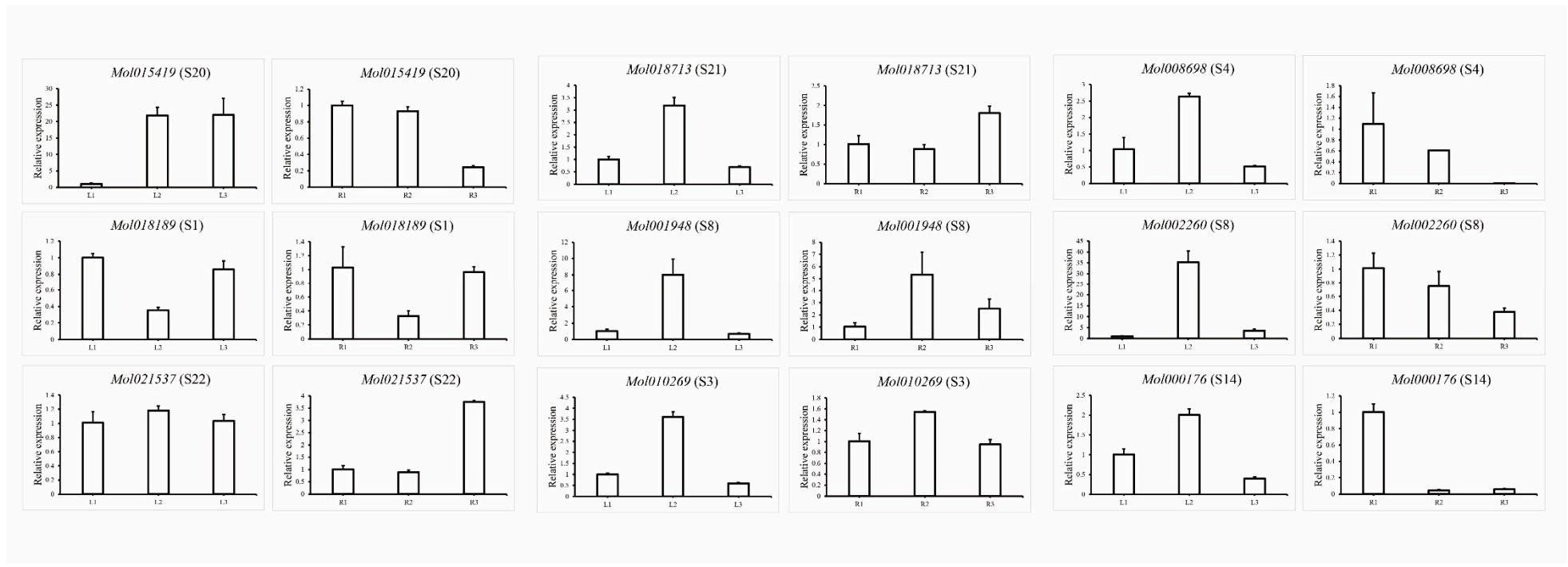
Gene ID	Primer name	Sequence
<i>Mol021537</i>	37-F	TCTAGCTCTACCAACCAAACCG
	37-R	TCCCGCTCAGATAATTCTCA
<i>Mol018189</i>	89-F	ACAGTCGTTACCATCGTCG
	89-R	TAGGCGGTTCTCATCCA
<i>Mol015419</i>	19-F	GGAAACCGCTGGTCAAAGA
	19-R	GGACGATGAGAACCCATTACG
<i>Mol002260</i>	60-F	TTGTTGTTGGCGGGCAGTA
	60-R	TCGGGGCGAAGATAGTTGT
<i>Mol018713</i>	13-F	ATTTCCTGGTCGCACAGATAAC
	13-R	AAACTGCCTTGCTTCCTTG
<i>Mol001948</i>	48-F	CAGGCTGAGATGGACGAACAT
	48-R	CGGTTCTTCCAGGGAGGTTT
<i>Mol008698</i>	98-F	CTCGGCAACAAATGGTCGT
	98-R	GCTGCTCTTGTTCCTTCGTCT
<i>Mol000176</i>	76-F	GGCTCCGATGGCTGAACAT
	76-R	TGATCTTGCAGGATTGC
<i>Mol010269</i>	69-F	AATAAGGGCTCATGGACGGT
	69-R	CGACAACCTTCCCACAACG
<i>Mol022529</i>	ACT-F	TGGCATCACACCTCTACAAC
	ACT-R	CATAGCAGGCACATTGAAAGTC



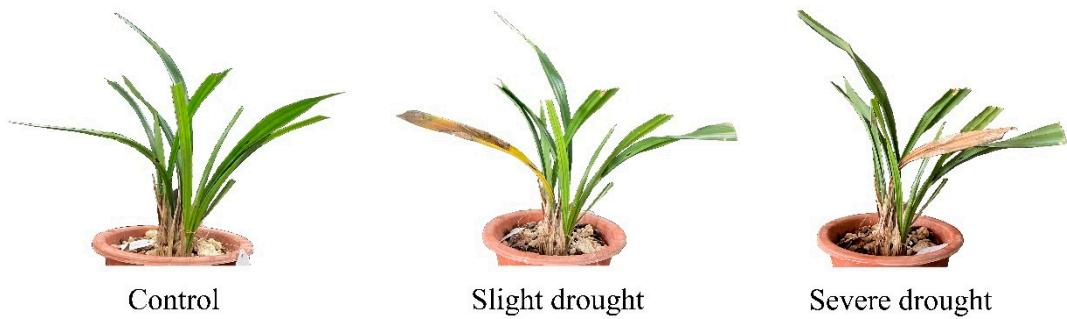
**FIGURE S1.** The 15 motifs of *CsMYBs* and *DrMYBs*



**FIGURE S2.** The collinearity of *CsMYB* genes in *C. sinensis*. The gray line in the background indicates collinear blocks within species, while the red lines highlight the syntenic R2R3-MYB gene pairs.



**Figure S3.** RT–qPCR validation of transcriptomic data of nine *CsMYB* genes under drought stress.



**FIGURE S4.** The plant of *C. sinense* under three treatments.